PCT WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 7 : C07H 21/04, A61K 48/00 — A2

(11) International Publication Number: **WO 00/56756**

(43) International Publication Date: 28 September 2000 (28.09.00)

(21) International Application Number: PCT/US00/07642

(22) International Filing Date: 23 March 2000 (23.03.00)

(30) Priority Data:
60/125,728 23 March 1999 (23.03.99) US

(71) Applicant *(for all designated States except US)*: MOUNT SINAI SCHOOL OF MEDICINE OF NEW YORK UNIVERSITY [US/US]; One Gustave L. Levy Place, New York, NY 10029–6504 (US).

(72) Inventors; and
(75) Inventors/Applicants *(for US only)*: BANCROFT, Carter, F. [US/US]; 51 Dewey Street, Huntington, NY 11743 (US). FLISS, Makiko [JP/US]; 6491 Lacelike Row, Columbia, MD 21045 (US). CLELLAND, Catherine, L. [GB/US]; Apartment 4A, 324 East 59th Street, New York, NY 10022 (US).

(74) Agents: KOLE, Lisa, B. et al.; Baker Botts LLP, 30 Rockefeller Plaza, New York, NY 10112–0228 (US).

(81) Designated States: CA, JP, US, European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE).

Published
With declaration under Article 17(2)(a); without abstract; title not checked by the International Searching Authority.

(54) Title: PROLACTIN REGULATORY ELEMENT BINDING PROTEIN AND USES THEREOF

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece			TR	Turkey
BG	Bulgaria	HU	Hungary	ML	Mali	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MN	Mongolia	UA	Ukraine
BR	Brazil	IL	Israel	MR	Mauritania	UG	Uganda
BY	Belarus	IS	Iceland	MW	Malawi	US	United States of America
CA	Canada	IT	Italy	MX	Mexico	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NE	Niger	VN	Viet Nam
CG	Congo	KE	Kenya	NL	Netherlands	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NO	Norway	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	NZ	New Zealand		
CM	Cameroon			PL	Poland		
CN	China	KR	Republic of Korea	PT	Portugal		
CU	Cuba	KZ	Kazakstan	RO	Romania		
CZ	Czech Republic	LC	Saint Lucia	RU	Russian Federation		
DE	Germany	LI	Liechtenstein	SD	Sudan		
DK	Denmark	LK	Sri Lanka	SE	Sweden		
EE	Estonia	LR	Liberia	SG	Singapore		

PROLACTIN REGULATORY ELEMENT BINDING PROTEIN AND USES THEREOF

SPECIFICATION

1. INTRODUCTION

The present invention relates to isolated nucleic acids encoding Prolactin Regulatory Element Binding (*PREB*) protein and recombinant proteins encoded thereby. The nucleic acid sequences are useful in the production of recombinant PREB, as probes, and in the control of prolactin gene expression. In particular embodiments of the invention, *PREB* nucleic acid sequences are used to detect transcripts of the gene in astrocytomas. The PREB protein is associated with the kinase-mediated hormonal regulation of prolactin gene expression, and may be used as a trans-acting control of transcription.

2. BACKGROUND OF THE INVENTION

2.1. FUNCTION OF THE PROLACTIN HORMONE

Prolactin (PRL) is an anterior pituitary hormone that is part of a family of hormones. Prolactin was discovered in 1928 based on the ability of pituitary extracts to cause lactation in pseudo-pregnant rabbits. Cooke, N.E., and Leibhaber, S. A., 1995, *Vitamins and Hormones* 50:385-459. Accumulated data now suggest a very broad spectrum of roles for PRL. PRL is linked to over three-hundred separate actions in vertebrates including effects on water and salt balance, growth and development, metabolism, brain behavior, reproduction, and immune regulation and protection. Bole-Feysot C. et al.,1998, *Endocr. Rev.* June; 19(3): 225-268. Additionally, a number of disease states, including the growth of different forms of cancer as well as various autoimmune diseases, appear to be related to an overproduction of PRL. Bole-Feysot C. et al., 1998, *Endocr. Rev.* June; 19(3): 225-268.

Studies have shown that female transgenic mice over-expressing the rat PRL gene all develop mammary carcinomas at 11-15 months of age and male transgenic mice over-expressing PRL develop dramatic enlargement of the prostate gland. Wennbo H. et al., 1997, *J. Clin. Invest.* December 1; 100 (11):2744-2751. The effect of PRL on cell proliferation was studied in a mouse mammary tumor cell line. The results of the study indicated that PRL antiserum is able to inhibit cell growth by 70% suggesting that PRL may be acting as a local growth factor that stimulates the proliferation of mammary tumors. Mersho, J. et al., 1995, *Endocrinology.* August; 136(8):3619-3623. Similarly, human breast cancer cells synthesize and secrete biologically active PRL and there is evidence to support that PRL may be involved in an autocrine/paracrine stimulatory loop within breast tissues that may play a role in the pathogenesis of breast cancer. Clevenger C.V. et al., 1995, *Am. J. Pathol.* March; 146(3):695-705.

In addition, PRL is produced by leukocytes and fibroblasts and animal model studies suggest that increased levels of serum PRL may influence the course of arthritis, lupus, and autoimmune type I diabetes, indicating that PRL may play a role in autoimmune diseases and the regulation of immune responses. Neidhart, M., 1998, *Proc. Soc. Exp. Biol. Med.* April; 217(4):408-419. Ferrag, F. et al., 1997, *Cytokines Cell Mol Ther.* Sep;3(3):197-213. Therefore, an important aspect of therapeutic approaches with respect to these diseases is the understanding of the regulation of PRL expression.

2.2. TISSUE SPECIFIC EXPRESSION OF PROLACTIN

The prolactin gene appears to function as an important element in tissue-specific and developmentally regulated gene expression. Cooke, N.E. and Liebhaber, S. A., 1995, *Vitamins and Hormones* 50:385-459. Prolactin is expressed in a cell-type specific fashion in pituitary lactotropic cells. Cooke, N.E. and Liebhaber, S. A., 1995, *Vitamins and Hormones* 50:385-459. In addition, prolactin expression has been found in human endometrial cells, human breast tissue, human mammary cell lines, human ovaries, human immune system cells and tissues (thymus, spleen, tonsil, lymph node, lymphocytes, and lymphoid tumors), epithelial cells, vascular

endothelial cells, hypothalamic cells, and in human decidua-chorion. Tanaka, S. et al., 1996, *Eur. J. Endocrinol.* 135(2):177-183; Shaw-Bruha, C. M., 1997, *Breast Cancer Res. Treat.* 44(3):243-253; Schwarzler, P. et al., 1997, *Fertil. Steril.* 68(4):696-701; Wu, H. et al., 1996, *Endocrinology* 137(1):349-353; Clapp, C. et al., 1994, *Proc. Natl. Acad. Sci. USA* 91(22):10384-10388; Clements, J., 1983, *Endocrinology* 112(3):1133-1134. Among human tissues which do not express prolactin are lung and kidney as well as many others. Schwarzler, P. et al., 1997, *Fertil. Steril* 68(4):696-701. Although it has been shown that prolactin is expressed in a tissue dependent manner, it is not clear which transcription factors are responsible. While Pit-1, the POU homeo-domain transcription factor (a variant of the helix-turn-helix type transcription factor), gene expression has been shown to follow levels of prolactin expression, Pit-1 is expressed in 3 cell types of the pituitary (thyrotropic cells, lactotropic cells, somoatotropic cells, somatolactortropic cells) while prolactin is primarily expressed in lactotropic cells. Crenshaw, E. B. et al., 1989, *Genes Dev.* 3(7):959-972. The mechanism of tissue specific expression of prolactin is still being investigated.

2.3. PRL REGULATION

Transcription factors are proteins that bind to regulatory elements in genes and have a critical role in gene regulation and protein expression during development, cellular growth and differentiation. Transcription factors generally can be categorized into four major groups according to the motif in their DNA-binding domains which include (1) the helix-turn-helix group, (2) the zinc finger group, (3) the leucine zipper group, and (4) the helix-loop-helix group. Lloyd, R.V. and Osamura, R.Y., 1997, *Microsc. Res. Tech.* 39(2):168-181.

The prolactin promoter contains multiple binding sites implicated in basal PRL expression and in kinase-mediated hormonal regulation of the gene. The pituitary-specific transcription factor Pit-1 has been shown to play an important role in the expression by the pituitary of the prolactin gene both in development and in the mature organism. Iverson, R.A. et al., 1990, *Mol. Endocrinol.* 4:1564-1571. Okimura, Y. et al., 1994, *Mol. Endocrinol.* 8:1559-1565. Although Pit-1 binds to

many of the binding sites in the PRL promoter, it does not appear to be responsible for kinase-mediated hormonal regulation of PRL. Fischberg, D.J. et al., 1994, *Mol. Endocrinol.* 8:1566-1573; Okimura, Y. et al., 1994, *Mol. Endocrinol.* 8:1559-1565; Howard, P.W. and Maurer, R.A., 1994, *J. Biol. Chem.* 269:28662-28669. This suggests that there are factors other than Pit-1 that are responsible for the regulation of PRL gene expression.

Oct-1 and TEF are two other transcription factors which can bind to the promoter of the PRL gene. Voss, J.W. et al., 1991, *Genes Dev.* 5:1309-1320; Drolet, D.W. et al., 1991, *Genes Dev.* 5:1739-1753. Studies show that Oct-1 is unlikely to be involved in the kinase-mediated transcription of the prolactin gene since protein kinase A (PKA)-mediated phosphorylation of Oct-1 decreases its DNA binding activity. Segil, N. et al., 1991, *Science* 254:1814-1816. Additionally, TEF is not likely to be involved in the kinase-mediated transcription of the prolactin gene since its mode of action is apparently limited to thyrotroph development.. Voss, J.W. et al., 1991, *Genes Dev.* 5:1309-1320.

Mutations in the *Pit1* gene, observed in the naturally occurring *Snell* (dw) and Jackson (dwJ) mutant mice, result in a murine phenotype of severe growth retardation and a remarkably hypoplastic pituitary gland, due to a developmental failure of the three anterior pituitary cell types that specifically express the hormones regulated by *Pit1*. *See* Li et al., *Nature* 347:528-533 (1990). Mutations in the human homologue of *Pit1* have also been shown to be responsible for deficiencies of these three pituitary hormones, and to result in a human phenotype of growth abnormalities, severe mental retardation, failure of lactation, congenital hypoparathyroidism, facial dysmorphism and hypoplastic pituitary. *See* Radovick et al, *Science* 57:1115-1118 (1992); Tatsumi et al., *Nat. Genet.* 1:56-58 (1992); de Zegher et al, *J. Clin. Endocr. Metab.* 80:3127-3130 (1995).

Despite evidence that PRL gene expression is highly regulated and induced by the cAMP-protein kinase-A pathway, a transcription factor involved in the kinase-mediated transcription of the prolactin gene has been, prior to the present invention, elusive. Keech, C.A. et al., 1992, *Mol Endocrinol* 6(12):2059-2070. Evidence suggests that there is a ubiquitous transcription factor that is involved in the

PKA-mediated transcriptional activation pathway of prolactin. Rajnarayan, S. et al., 1995, *Mol Endocrinol* 9(4):502-512. A better understanding of the PKA-mediated transcriptional activation pathway, coupled to more effective means to control this pathway, could lead to the treatment of ailments that are related to the inappropriate expression of the prolactin gene.

2.4. TREATMENT OF DISEASE THROUGH PROLACTIN REGULATION

Since its discovery in 1928, PRL has been implicated in a broad spectrum of roles including regulation of reproductive function, control of metabolism, osmoregulation, and immune regulation, as well as growth and development in certain vertebrate species. Nicoll, C. S., 1991, *Perspect. Biol. Med.* 25:369-381. In addition to becoming well known as an important regulator of immune function, a number of disease states, including different forms of cancer, autoimmune diseases, developmental diseases and osteoporosis have been connected to the overproduction of PRL. Yu-Lee, L-y., 1997, *Proc. Soc. Exp. Biol. Med.* 215:35-52; Adler et al., *Metabolism*, 47:425-428 (1998).

PRL expression has been detected in human mammary tumors, and human mammary tumor cell lines can produce PRL, indicating a possible auto/paracrine function of PRL in mammary tumor growth. Wennbo, H. et al., 1997, *J. Clin. Invest.* 100:2744-2751. In addition, inhibitors of the proliferation of human breast cancer cells *in vitro* appear to inhibit endogenous prolactin action at the level of the prolactin receptor and antibodies to PRL inhibit the proliferation of rat mammary tumor cells *in vitro*. De Petrocellis, L. et al., 1998, *Proc Natl. Acad. Sci. USA* 95(14):8375-8380; Mersho, J. et al., 1995, *Endocrinology* 136(8):3619-3623. Furthermore, tamoxifen, an anti-estrogen which is known for its anti-tumoral action *in vivo*, inhibits PRL-induced activation of kinases as well as PRL binding and cell growth indicating the possible role of PRL inhibition in the treatment of breast cancer. Das, R. and Vonderhaar, B. K., 1997, *Cancer Letters* 116(1):41-46. Another study aimed at further characterizing the role of prolactin in breast cancer has focused on the creation of transgenic mice that over-express prolactin. Significantly, all of the female mice which over-expressed PRL developed mammary carcinomas at 11-15 months of

age. Wennbo, H. et al., 1997, *J. Clin. Invest.* 100:2744-2751. In the same study, organ culture experiments were conducted which demonstrated an autocrine/paracrine effect of PRL.

The role of PRL in human breast cancer has been suggested in a study that reports two cases of breast cancer associated with prolactinoma. Strungs, I. et al., 1997, *Pathology* 29(3):320-323. Correspondingly, male mice which over-expressed PRL developed dramatic enlargement of the prostate gland, approximately 20 times the normal size. Wennbo, H. et al., 1997, *Endocrinology* 138(10)4410-4415. It is interesting to note that the level of PRL increases with age, coinciding with development of prostate hyperplasia in humans. Hammond, G. L. et al., 1997, *Clin. Endocrinol.* 7:129-135. It appears therefore that PRL may be an important factor in the etiology of prostate diseases including cancer. All the aforementioned studies are in strong support of the notion that PRL may be an important target in the quest to control cancer.

PRL has also been implicated in autoimmune diseases. PRL, as well as growth hormone, is required for the development of mature lymphocytes and for the maintenance of immunocompetence. Berczi, I., 1997, *Acta Paediatr Suppl.* 423:70-75. It is suggested that hyperprolactinemia is a risk factor for the development of autoimmunity. There are many studies that support a role of PRL in modulating the immune response and altered PRL levels have been observed in animal models of autoimmune diseases such as lupus erythematosus, diabetes, rheumatoid arthritis, and collagen type II-induced arthritis. Berczi, I., 1983, et al. *Acta. Endocrinol.* 102:351-357; Jara, L. J. et al., 1992, *Am. J. Med. Sci.* 303:222-226; Neidhart, M., 1998, *Proc. Soc. Exp. Biol. Med.* 217(4):408-419. Since PRL constitutes a stimulatory link between the neuroendocrine and immune systems, increased serum levels may activate a hyperimmune response. Neidhart, M., 1998, *Proc. Soc. Exp. Biol. Med.* 217(4):408-419. In these diseases, it may be advantageous to reduce the serum levels of PRL by inhibiting its gene expression. Additionally, serum PRL levels were elevated in human bone transplantation patients which exhibited chronic graft-versus-host disease indicating that prolactin is a mediator of graft-versus-host disease. Hinterberger-Fischer, M. et al., 1994, *Bone Marrow Transplant* 14(3):403-406. The

inhibition of PRL after transplantation may decrease the rejection problems of transplantation patients.

In contrast, an increase in prolactin expression may be beneficial where the immune response is compromised, for example, in AIDS. Recombinant human PRL has been demonstrated to have the ability to stimulate proliferation of B-cell hybridomas in a dose-dependent manner, resulting in an overall increase of antibody production. Richards, S.M. et al., 1998, *Cell. Immunol.* 184(2):85-91. Additionally, PRL was able to overcome the growth inhibition of the hybridoma cells by transforming growth factor beta (TGF-beta), indicating a role for PRL in the treatment of diseases associated with over-expression of TGF-beta, or in AIDS where it may be advantageous to stimulate lymphoid cells. Hinterberger-Fischer, M. et al., 1994, *Bone Marrow Transplant* 14(3):403-406.

PRL may regulate bone marrow function as well. In rats which have their pituitary gland removed, treatments with PRL reversed the anemia, leucopenia, and thrombocytopenia in their bone marrow. Nagy, E. and Berczi, I., 1989, *Br. J. Haematol.* 71(4):457-462. Moreover, prolactin regulation of the growth of hematopoetic progenitors in a bone marrow stroma environment has been demonstrated *in vitro* by the addition of PRL antibodies to cultures resulting in a reduction of hematopoetic progenitor colonies. Bellone, G., 1997, et al. *Blood* 90(1):21-27. These findings suggest that over-expression of prolactin may be used to stimulate the growth of hematopoetic progenitor cells *in vitro* which may ultimately be transplanted into a patient.

Studies have also linked PRL overproduction with osteoporosis. Humans with prolactinoma are at risk for reproductive disorders and osteoporosis which may be due to PRL-induced hypogonadism. *See* Adler et al., *Metabolism* 47:425-428 (1998). In addition, anovulation condition (which is an estrogen deficiency due to high prolactin levels) is linked with premature bone mass loss. *See* Koloszar et al., *Orv. Hetil.* 138:71-73 (1997). It has been suggested that osteopathy in hyperprolactinemic hypogonadism is due to reduced bone formation and not reduced estradiol production, indicating a link of PRL levels with bone formation. *See* Rozhinskaia et al., *Probl. Endokrinol.* 38:17-19 (1992). Similarly, Ciccarelli et al.

(*Clin. Enndocrinol.* 28:1-6 (1988)) have suggested that there is a direct effect of PRL on bone mass. The risk of developing osteoporosis due to increased levels of PRL has been seen in women as well as in men. *See* Jackson et al., *Ann Intern. Med.* 105:543-545 (1986).

3. SUMMARY OF THE INVENTION

The present invention relates to the discovery of a novel transcription factor, called PREB (Prolactin Regulatory Element Binding) protein which functions in the kinase-mediated hormonal regulation of prolactin gene expression. The invention is based, at least in part, on the discovery and characterization of the rat *Preb* gene and protein and the identification of a cloned human DNA containing the human *PREB* gene.

In a first series of embodiments, the present invention provides for a nucleic acid molecule encoding *PREB*, and a PREB protein having an amino acid sequence as encoded by that nucleic acid which binds to the 1P element of the PRL promoter.

In a second set of embodiments, the present invention provides for a method of inhibiting kinase-mediated transactivation of prolactin gene expression.

In a third set of embodiments, the present invention provides for an assay for distinguishing between different brain tumor types whereby PREB transcript levels are quantified. For example, but not by way of limitation, PREB transcript levels can be quantified using a *PREB* nucleic acid sequence as a probe, by RT-PCR analysis or by microarray analysis. The presence of *PREB* would indicate the presence of astrocytoma brain tumor cells but not neuroepithelioma or glioma brain tumor cells.

In a fourth set of embodiments, the present invention provides for methods for the treatment of cancers and autoimmune diseases through the inhibition of prolactin gene expression.

In a fifth set of embodiments, the present invention provides for methods for improving the immune response by increasing prolactin gene expression.

In a sixth set of embodiments, the present invention provides for a method for inhibiting Pit-1-mediated transactivation of prolactin gene expression and the transactivation of other genes whose transcriptional activation is controlled by Pit-1.

In a seventh set of embodiments, the present invention provides for methods for stimulating the growth of cells both *in vitro* and *in vivo* through the over-expression of genes by the use of promoter sequences which are regulated by the binding of the PREB transcription factor. This method is also useful in the culture of skin cells or bone marrow cells *in vitro* which will ultimately be transplanted into a patient.

In an eighth set of embodiments, the present invention provides for a method for inhibiting graft-versus-host disease in transplant patients through the inhibition of prolactin gene expression.

In a ninth set of embodiments, the present invention provides for a method for controlling development through the inhibition of PREB expression.

In a tenth set of embodiments, the present invention provides for a nucleic acid encoding human *PREB*, as contained in plasmid pCRScript (Stratagene) deposited with the American Type Culture Collection (10801 University Blvd., Manassas, VA 20110-2209 USA) and assigned accession number PTA1259. The present invention also provides for two genomic fragments, which encompass the PREB gene minus 500 bp from the 3' UTR that is within the cDNA transcript, of 1.6 kb and 2.5 kb respectively, which were deposited with the American Type Culture Collection (10801 University Blvd., Manassas, VA 20110-2209 USA) and assigned accession numbers PTA1258 and PTO1260 respectively.

In an eleventh set of embodiments, the present invention provides for a method of detecting trisomy 2p whereby a *PREB* nucleic acid sequence is used as a probe. The presence of additional copies of *PREB* would indicate a trisomy 2p condition.

In a twelfth set of embodiments, the present invention provides for a method of detecting an increased propensity to develop osteoporosis whereby any change in the expression of PREB which results in activation or inactivation of the

PREB protein would indicate a propensity to develop osteoporosis. For example, changes which could indicate an increased propensity to develop osteoporosis include, but are not limited to, (1) changes in the *PREB* gene, such as heterozygous or homozygous partial or total deletions of the *PREB* gene, insertions, base pair changes, mutations, etc.; (2) changes in the transcript levels; and/or (3) changes in the PREB protein levels and truncations of the PREB protein (which may be the result of a mutation in the *PREB* gene) which could result in an up-regulation of certain pathways.

In a thirteenth set of embodiments, the present invention provides for a method of treating osteoporosis, or lowering the likelihood of developing osteoporosis comprising administering the *PREB* gene or gene product, including, but not limited to antisense *PREB* mRNA, or the PREB protein, to a subject.

4. DESCRIPTION OF THE FIGURES

FIGURE 1 A & B. (A) a map of the protein; (B) nucleic acid sequence of rat *Preb* cDNA (SEQ ID NO:1) and deduced amino acid sequence (SEQ ID NO:2).

FIGURE 2. Nucleic acid sequence of *Homo sapiens* cDNA clone R12741 (SEQ ID NO:3).

FIGURE 3 A-C. DNA target site for *PREB*. (A) Partially purified poly-His-tagged PREB (40 ng) protein was incubated with a ^{32}[P]-site 1P probe, plus or minus excess (50-250 fold) of the indicated competitors, and analyzed on polyacrylamide gels. Lane 1 received no added protein, and lanes 1-11 and 12-23 were analyzed on separate gels. To improve resolution, the free probe was run off the end of the gel. The single major shifted band observed with PREB is indicated. (B) Structure of site 1P and sequences mutated in competitors *1P and 1P*, and region predicted to form part of the binding site for PREB. The bases shown by X-ray crystallography structure analysis to be contacted by Pit-1 POU domain dimers (Jacobson et al. *Genes Dev.* 11:198-212. 1997) are bracketed. (C) Schematic of nucleotide sequences of 1P, *1P, 1P*, *1P*, and 3P.

FIGURE 4 A-D. Southern blot analysis of the *PREB* gene in various organisms (A) Rat, (B) Human, (C) Drosophila, and (D) Yeast. DNA isolated from

the organisms was digested with the indicated restriction enzymes, and subjected to Southern blot analysis, employing a *PREB* cDNA probe. Hybridization was at reduced stringency (39°C), except for rat DNA, where stringent conditions were employed. The sizes of internal DNA molecular weight markers are indicated.

FIGURE 5 A - D. Size and nuclear accumulation of PREB in GH3 cells. (A) Nuclei and cytosol were prepared, and the nuclei extracted with 0.42 mM KCl. Nuclear and cytosolic proteins from an equal number of cells were then analyzed on a Western blot, employing anti-PREB antiserum. Sizes of marker proteins on the same gel are indicated. The same antiserum was employed for immunocytochemistry of (B) GH3 cells with Antibody, (C) GH3 cells with pre-immune serum or (D) C6 cells. Ab, anti-PREB antiserum; Pre, preimmune serum from the same animal.

FIGURE 6. PREB can transactivate expression directed by the prolactin promoter plus enhancer. C6 rat glial cells ($2.6x10^6$) were electroporated with (-1957) PRL-CAT (10 μg) plus RSV-βgal (2 μg), plus 5 μg either RcRSV ("None"), or RSV-Pit-1 or RSV-PREB, divided into three 60 mm dishes, incubated two days, and then assayed for CAT and β-galactosidase activity. Shown is the mean ± standard deviation (SD) of CAT activity, corrected for β-galactosidase activity, observed with triplicate dishes.

FIGURE 7 A & B. PREB and Pit-1 yield equivalent activation of expression of prolactin promoter construct. (A) Structure of plasmid (-113)PRL-CAT, illustrating the positions of the known prolactin promoter elements. (B) C6 cells ($2.6x10^6$) were electroporated with (-113)PRL-CAT (10 μg) and RSV-βgal (2 μg), plus the indicated amounts of either RSV-Pit-1 or RSV-PREB, and treated thereafter as in Figure 6. Shown is the mean ± SD of corrected CAT activity observed with triplicate dishes.

FIGURE 8. PREB and Pit-1 exhibit additive stimulation of a prolactin promoter construct. C6 cells were electroporated with (-113)PRL-CAT and RSV-βgal as in Figure 7, plus the indicated amounts of RSV-PREB and/or RSV-Pit-1 (1 = 2.5 μg plasmid), and treated thereafter as in Figure 6. Shown is the mean ± SD of corrected CAT activity observed with triplicate dishes.

FIGURE 9. PREB can support a PKA-mediated transcriptional response in pituitary cells. GH_3 rat pituitary cells were electroporated with 5XGAL4-CAT (10 μg) and RSV-βgal (2 μg), plus 5 μg either pGAL4 (1-147) or GAL4-PREB, plus 5 μg either RcRSV (PKA-) or RSV-PKA (PKA+) and treated thereafter as in Figure 6. Shown is the mean ± SD of corrected CAT activity observed with triplicate dishes.

FIGURE 10. PREB, but not Pit-1, can mediate regulation by PKA of expression of a prolactin promoter construct. C6 cells were electroporated with (-113)PRL-CAT and RSV-βgal as in Figure 7, plus 2.5 μg either RcRSV (None), RSV-Pit-1 or RSV-PREB, plus 5 μg either RcRSV (PKA-) or RSV-PKA (PKA+), and treated thereafter as in Figure 6. Shown is the mean ± SD of corrected CAT activity observed with triplicate dishes.

FIGURE 11. Nucleic acid sequence of human *PREB* cDNA (SEQ ID NO:12) and deduced amino acid sequence (SEQ ID NO:13).

FIGURE 12. Species conservation of the PREB WD-repeat Motifs. All amino acids that fall within the WD-repeat consensus are shaded.

FIGURE 13 A-D. Human *PREB* gene expression. (A) Key to the human tissue sources represented on the RNA master blot (Clonetech). The mRNA samples in rows A-F originate from 43 adult tissues ; samples in row G are derived from seven human fetal tissues; row H contains negative control RNA and DNA samples. (B) Control ubiquitin cDNA hybridization to the RNA filter. (C) Northern analysis with a 350 bp human *PREB* 3' UTR fragment probe. (D) A shorter exposure of the *PREB* probe hybridization shown in panel C showing variation among tissues in the levels of PREB expression in adult salivary gland, liver, pancreas and skeletal muscle, and fetal liver tissue.

FIGURE 14 A-G. FISH mapping and dosage analysis of *PREB*. (A) Mapping of the human *PREB* gene to chromosome 2 by FISH using metaphase chromosomes from normal male lymphocytes. (B) Regional assignment of the FISH signals to 2p23. (C) Metaphase chromosomes from patient A with t(2,11)(p21; q23.3). (D) Metaphase chromosomes from the cell line GM04409 derived from a patient with t(2;14)(p23;q32). (E) Metaphase chromosomes from patient B with

t(2;13)(p23;p11.2). (F) Interphase nuclei from the cell line GM04409. (G) Interphase nuclei from patient B.

FIGURE 15 A & B. (A) Nucleic acid sequence of human *PREB* alternative splice variant cDNA (SEQ ID NO:16) and (B) deduced amino acid sequence (SEQ ID NO:17).

FIGURE 16. Genomic nucleic acid sequence of the human *PREB* gene. Bold-face type indicates exons and nonbold-faced type indicates introns.

5. DETAILED DESCRIPTION OF THE INVENTION

For purposes of clarity of description, and not by way of limitation, the detailed description of the invention is divided into the following subsections:

(i) the *PREB* gene and its products;

(ii) diagnostic methods;

(iii) regulation of prolactin gene expression;

(iv) PREB and osteoporosis propensity;

(v) methods of treatment; and

(vi) expression of foreign genes.

5.1 *PREB* GENE AND ITS PRODUCTS

The present invention relates to nucleic acid molecules which encode a PREB protein capable of increasing expression of prolactin in a pituitary cell., including RNA, DNA, any cDNA or antisense counterparts thereof and any complementary nucleic acid sequences. In particular nonlimiting embodiments, the present invention provides for (i) a nucleic acid molecule having a sequence as set forth in SEQ ID NO:1, SEQ ID NO:12, or SEQ ID NO:16; (ii) a nucleic acid molecule which encodes a protein having a sequence as set forth in SEQ ID NO:2, SEQ ID NO:13, or SEQ ID NO:17; (iii) and nucleic acid molecules which hybridize to a nucleic acid molecule of (i) or (ii) under stringent hybridization conditions as set forth below, and which encode a protein that binds to the 1P element of the PRL promoter such that binding results in transactivation of the PRL gene. Stringent hybridization conditions as defined herein include conditions for prehybridization and hybridization,

performed at 39° C, according to the Basic Protocol described in Ausubel et al (*Short Protocols in Molecular Biology*, Third Edition, 1995, John Wiley and Sons, Publisher), Unit 2.10, employing a ^{32}[P] random-primed rat *Preb* cDNA probe and the aqueous prehybridization/hybridization (APH) solution described in *Short Protocols in Molecular Biology* (Appendix 1), and washing of filters as described in *Short Protocols in Molecular Biology*, Unit 2.10, including the two optional 15 minute moderate-stringency washes described (42° C. 0.2xSSC/0.1% SDS).

The term "*PREB* gene", as used herein, collectively includes the rat *Preb* gene, its human counterpart (*PREB*) homologs thereof in other species which are at least ~ 85%, and preferably ~95%, homologous to the complete rat *Preb* gene (homology determined by Blast Search Algorithm; Netscape Navigator, 3.01), and alternatively spliced variants of PREB.

In one specific nonlimiting embodiment, the invention provides for a human *PREB*-encoding nucleic acid sequence as set forth in Figure 2 (SEQ ID NO:3), which hybridizes to a nucleic acid sequence having SEQ ID NO:1 under stringent hybridization and wash conditions as set forth above, and which human PREB protein encoded thereby binds the human PRL promoter wherein such binding transactivates PRL gene transcription. In a further nonlimiting embodiment, the invention provides for human *PREB*-encoding nucleic acid sequences as set forth in Figure 11A (SEQ ID NO:12) and Figure 15A (SEQ ID NO:16) and the deduced amino acid sequence (SEQ ID NO:13 and SEQ ID NO:17, respectively). The *PREB* gene of the present invention is involved in PRL regulation and also functions as a DNA-binding transcription factor during mammalian development.

The present invention also provides for PCR primers which may be used to prepare cDNA or genomic DNA corresponding to all, or part of the *PREB* gene as set forth in the example section below. Such techniques may be used to identify and isolate a nucleic acid molecule encoding the entire PREB protein or mutants thereof.

In a specific, nonlimiting embodiment, the present invention provides for a substantially purified nucleic acid molecule containing a rat *Preb* encoding cDNA, which has a nucleic acid sequence designated as SEQ ID NO:1 and an amino

acid sequence designated as SEQ ID NO:2. The invention also provides for a substantially purified nucleic acid molecule containing a human *PREB*-encoding cDNA, which has a nucleic acid sequence designated as SEQ ID NO:12 or SEQ ID NO:16 and an amino acid sequence designated as SEQ ID NO:13 or SEQ ID NO:17.

The *PREB* gene or corresponding cDNA or RNA or any corresponding complementary or anti-sense nucleic acid molecule may be incorporated into any suitable cloning or expression vector, operably linked to appropriate control elements (e.g. promoter elements, enhancer elements, ribosomal binding sites, polyadenylation sites, termination sites, etc.). Examples of such vectors include, but are not limited to, herpes simplex viral based vectors such as pHSV1 (Geller et al., 1990, *Proc. Natl. Acad. Sci.* U.S.A. 87:8950-8954); retroviral vectors such as MFG (Jaffee et al., 1993, *Cancer Res.* 53:2221-2226), and in particular Moloney retroviral vectors such as LN, LNSX, LNCX, LXSN (Miller and Rosman, 1989, *Biotechniques* 7:980-989); vaccinia viral vectors such as MVA (Sutter and Moss, 1992, *Proc. Natl. Acad. Sci.* U.S.A. 89:10847-10851); adenovirus vectors such as pJM17 (Ali et al., 1994, *Gene Therapy* 1:367-384; Berker, 1988, *Biotechniques* 6:616-624; Wand and Finer, 1996, *Nature Medicine* 2:714-716); adeno-associated virus vectors such as AAV/neo (Mura-Cacho et al., 1992, *J. Immunother.* 11:231-237); lentivirus vectors (Zufferey et al., 1997, *Nature Biotechnology* 15:871-875); and plasmid vectors such as pCDNA3 and pCDNA1 (InVitrogen), pET11a, pET3a, pET11d, pET3d, pET22d, pET12a and pET28a (Novagen); plasmid AH5 (which contains the SV40 origin and the adenovirus major late promoter), pRC/CMV (InVitrogen), pCMU II (Paabo et al., 1986, *EMBO J.* 5:1921-1927), pZipNeo SV (Cepko et al., 1984, *Cell* 37:1053-1062), pSRα (DNAX, Palo Alto, CA) and pBK-CMV, pSPTg.T2FpAXK and pSPTg.2FXK (Schaleger et al., 1997, *Proc. Natl. Acad. Sci.* U.S.A. 94:3058-3063).

In specific non-limiting embodiments of the invention, a *PREB* gene or a corresponding cDNA or RNA may be comprised in an expression vector in frame with a second nucleic acid molecule encoding a second protein sequence so as to encode for a fusion protein in which *PREB* is positioned either C-terminal or N-terminal to the other gene. For example, the second nucleic acid molecule may encode a protein which, when fused with PREB, does not effect the DNA binding

activity of PREB but inhibits the DNA binding of other transcription factors which bind to PRL promoter elements in close proximity to PREB (*e.g.* glutathione-s-transferase, maltose-binding protein, etc). A dominant-negative fusion protein consisting of a transcriptionally defunct PREB fused to the POU DNA binding domain of Pit-1 is also within the scope of the invention. This PREB-Pit-1 fusion may be capable of binding cooperatively to the 1P element with an increased binding affinity as compared to either PREB or Pit-1 alone and may be capable of inhibiting the transactivation of PRL by endogenous PREB and Pit-1. The PREB protein sequence contains two putative transactivation domains (residues 86-134 and 223-279) whose amino acid sequences are rich in proline and glutamine. Proline-rich and glutamine-rich transactivation motifs have been identified in transcription factors. Mitchell, P.J. and R. Tjian, 1989, *Science* 245:371-378. Mutations in these regions, especially deletions of 10 to 20 amino acid residues, may result in a transactivationally defunct PREB protein which may be fused to another protein as described above.

The human PREB-encoding nucleic acids of the present invention were deposited with the American Type Culture Collection (ATCC), 10801 University Blvd., Manassas, VA 20110-2209, on February 1, 2000 and given accession numbers PTA-1258, PTA-1259 and PTA-1260. The human cDNA, as contained in plasmid pCRScript (Stratagene), was assigned accession number PTA1259. The present invention also provides for two genomic fragments, which encompass the PREB gene minus 500 bp from the 3' UTR that is within the cDNA transcript, of 1.6 kb and 2.5 kb respectively, which were assigned accession numbers PTA1258 and PTO1260 respectively.

In other specific, nonlimiting embodiments of the invention, an expression vector may incorporate a *PREB* gene (or a corresponding cDNA or RNA) as part of a polycistronic expression cassette together with a second gene whereby the second gene is operably linked to the 1P element of the PRL promoter and hence transactivated by PREB. For example, the second gene may encode for a protein capable of promoting cell growth, or capable of inhibiting the progression of cancer.

In further nonlimiting embodiments of the invention, the *PREB* gene may be co-expressed with another gene whereby the second gene is operably liked to

the 1P element of the PRL promoter and hence transactivated by PREB and whereby the *PREB* gene and the second gene are not part of the same expression vector.

In yet further, nonlimiting embodiments of the invention, an expression vector may comprise a *PREB* gene (or corresponding cDNA or RNA) operably linked to a heterologous promoter (*i.e.* a promoter other than the naturally occurring *PREB* promoter), wherein such heterologous promoter may be an inducible promoter (*e.g.* the metallothionine promoter).

The PREB protein encoded by the *PREB* gene of the present invention has significant sequence similarity with the yeast TUP1 transcriptional repressor protein (Accession No:p16649) and Pfam database screening has identified PREB as a WD-repeat family member.

Sequencing of the cDNA of *PREB* revealed that it encodes a protein with significant homology to several previously identified ESTs (AA538253 mouse clone from pooled mouse organs = 98% identity over 627 bp of 1919 bp, AI012746 rat placenta clone = 97% identity over 450 bp of 1919 bp, AA688602 mouse myotube clone = 96% identity over 476 bp of 1919 bp, AA647012 mouse mammary gland clone = 94% identity over 385 bp of 1919 bp, AA892136 rat kidney clone = 98% identity over 400 bp of 1919 bp, AA250620 mouse NML clone = 96% identity over 412 bp of 1919 bp, AA646576 mouse mammary gland clone = 96% over 399 bp of 1919 bp, AA967116 mouse mammary gland = 94% identity over 484 bp of 1919 bp, AA925797 rat kidney clone = 100% identity over 324 bp of 1919 bp, W30204 mouse clone = 95% identity over 424 bp of 1919 bp, AA792848 mouse myotube clone = 96% identity over 325 bp of 1919 bp, AA066564 mouse diaphragm clone = 100% identity over 293 bp of 1919 bp, AA111707 mouse clone = 90% identity over 497 bp of 1919 bp, H34594 rat clone = 95% identity over 276 bp of 1919 bp, AA351639 infant brain *Homo sapiens* clone = 88% identity over 386 bp of 1919 bp, AA300144 uterus tumor in *Homo sapiens* clone = 90% identity over 285 bp of 1919 bp, W04666 fetal lung *Homo sapiens* clone = 90% identity over 393 bp of 1919 bp, AA324676 cerebellum II *Homo sapiens* clone = 87% identity over 328 bp of 1919 bp, AA687138 *Homo sapiens* clone = 89% identity over 409 bp of 1919 bp, AA889019 parathyroid tumor *Homo sapiens* clone = 89% identity over 407 bp of 1919 bp, H83961 *Homo*

sapiens clone = 89% identity over 400 bp of 1919 bp, N75291 *Homo sapiens* clone = 89% identity over 400 bp of 1919 bp, AI089337 pregnant uterus *Homo sapiens* clone = 89% identity over 381 bp of 1919 bp, AA629936 Stratagene lung carcinoma *Homo sapiens* clone = 89% identity over 292 bp of 1919 bp, AA580861 *Homo sapiens* clone = 89% identity over 281 bp of 1919 bp, Z17827 Stratagene cDNA human heart library = 89% identity over 224 bp of 1919 bp, R39793 *Homo sapiens* clone = 89% identity over 450 bp of 1919 bp).

The ESTs show that *PREB* DNA is present in a number of organisms and in a number of tissues. Additionally, *PREB* DNA sequences are significantly conserved (> 85% homology overall). Although the ESTs span a significant portion of the *PREB* sequence as disclosed here, they have not been functionally defined and they do not represent a full length equivalent of *PREB*, with the largest EST spanning only 32.7% of the *PREB* sequence. In the absence of the full length clone and a functional characterization of the ESTs, these sequences have not disclosed the transcription factor which is responsible for the kinase-mediated transcriptional activation of prolactin and which has been elusive prior to the current invention.

The human *PREB* gene (Genbank Accession #AF203687) has been described (December 21, 1999). The human PREB protein and *PREB* gene with Accession Number AF203687 differ from the present invention by the following:

13 additional nucleotides at the 5' UTR (TGG CAA CTC CCC G)

Nucleic acid 408 C to A;

Nucleic acid 943 C to G;

Nucleic acid 949 C to G.

Nucleic acid 2045, insertion of T.

The present invention still further provides for purified and isolated PREB proteins, or analogs thereof including the rat and the human protein, having an amino acid sequence as set forth in Figure 1B (SEQ ID NO:2) and Figure 11B (SEQ ID NO:13), respectively. In addition, the present invention provides proteins encoded by the nucleic acids provided herein, including nucleic acids which hybridize to a nucleic acid having SEQ ID NO:1, SEQ ID NO:12, and/or SEQ ID NO:16 under stringent conditions, and proteins which are at least 85%, and preferably 90%

homologous to the complete rat or human PREB protein as determined by the Blast Search Algorithm and BESTFIT, through the program GCG (at HGMP, Cambridge, UK) using a Gap Weight of 8 and a Length Weight of 2. Correspondingly, human *PREB,* SEQ ID NO:12 encodes a 417 amino acid peptide and human *PREB* alternatively spliced variant, SEQ ID NO:16 encodes a 351 amino acid peptide.

In specific, non-limiting embodiments, the aforementioned peptides include the *PREB* gene's encoded protein including a start site at position 1 or a start site at position 217 as set forth in Figure 1B (SEQ ID NO:1) for the Rat *PREB* gene and position 144 and 272 (SEQ ID NO:12) for the Human *PREB* gene, giving rise to a 345 amino acid and a 417 amino acid peptides respectively.

The present invention further provides for PREB protein and peptides having altered sequences which do not affect the DNA binding activity and/or the transactivation activity of the protein. Also included within the scope of the invention are PREB protein or derivatives thereof which are modified pre- or post-translation, for example by glycosylation, RNA splicing, proteolytic cleavage, adenylation, phosphorylation, acetylation, linkage to a ligand or an antibody, etc..

The present invention also provides for PREB protein and peptides having altered sequences that do not effect the DNA binding activity of the protein to the 1P promoter but do effect the transactivation activity, either by inhibiting or stimulating the transactivation activity. Also within the scope of the invention are alterations of the amino acid sequences which improve DNA binding affinity.

The present invention further provides for PREB protein and peptides having altered sequences which abolish its transactivation activity and such protein and peptides being fused to another protein (*e.g.* see above) which can act to block nearby promoter sequences from binding other transactivating proteins. Such fusion proteins may block the binding of Pit-1 to the 1P element and nearby sequences thereby inhibiting Pit-1 transcriptional activation.

The present invention further provides for antibody molecules which specifically bind to a PREB protein, or portion thereof. According to the invention, a PREB protein, its fragments or other derivatives (*e.g.* histidine tagged protein), or analogs thereof, may be used as an immunogen to generate antibodies. Such

antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, Fab fragments, and a Fab expression library. In specific embodiments, antibodies which recognize rat PREB or a human homolog are produced. In nonlimiting specific embodiments, the antibodies which bind to PREB include, but are not limited to, a rabbit polyclonal antisera whereby a PREB peptide fragment (PREB amino acids 175-417, preceded by six histidines) is utilized as the immunogen to generate the antisera as described in the Examples section below.

Various procedures known in the art may be used for the production of polyclonal antibodies which specifically bind to a PREB protein. In a particular embodiment, rabbit polyclonal antibodies to an epitope of a PREB protein having an amino acid sequence set forth in FIGURE 1B (SEQ ID NO:2) or Figure 11B (SEQ ID NO:13) may be obtained. For the production of antibody, various host animals can be immunized by injection with the native PREB protein, or a synthetic version, or derivative (e.g., fragment) thereof, including but not limited to rabbits, mice, rats, goats, etc. Various adjuvants may be used to increase the immunological response, depending on the host species, and including but not limited to Freund's (complete or incomplete) adjuvant, mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanins, dinitrophenol, and potentially useful human adjuvants such as BCG (Bacille Calmette-Guerin) and *Corynebacterium parvum*.

For preparation of monoclonal antibodies directed toward a PREB protein, any technique which provides for the production of antibody molecules by continuous cell lines in culture may be used. Examples of such techniques include the hybridoma technique originally developed by Kohler and Milstein (1975, *Nature* 256:495-497), as well as the trioma technique, the human B-cell hybridoma technique (Kozbor et al., 1983, *Immunology Today* 4:72), and the EBV hybridoma technique to produce human monoclonal antibodies (Cole et al., 1985, in Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc., pp. 77-96). In an additional embodiment of the invention, monoclonal antibodies can be produced in germ-free animals utilizing recent technology (PCT/US90/02545). According to the invention, human antibodies may be used and can be obtained by using human hybridomas (Cote et al., 1983, *Proc.*

Natl. Acad. Sci. U.S.A. 80:2026-2030) or by transforming human B cells with EBV virus *in vitro* (Cole et al., 1985, in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, pp. 77-96). Further, according to the invention, techniques developed for the production of "chimeric antibodies" (Morrison et al., 1984, *Proc. Natl. Acad. Sci.* U.S.A. 81:6851-6855; Neuberger et al., 1984, *Nature* 312:604-608; Takeda et al., 1985, *Nature* 314:452-454) by splicing the genes from a mouse antibody molecule specific for *PREB* together with genes from a human antibody molecule of appropriate biological activity may be used; such antibodies are within the scope of this invention.

According to the invention, techniques described for the production of single chain antibodies (U.S. Patent 4,946,778) may be adapted to produce PREB-specific single chain antibodies. An additional embodiment of the invention utilizes the techniques described for the construction of Fab expression libraries (Huse et al., 1989, *Science* 246:12751281) to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity for PREB protein derivatives, or analogs.

Antibody fragments which contain the idiotype of the molecule can be generated by known techniques. For example, such fragments include but are not limited to: the $F(ab')_2$, fragment which can be produced by pepsin digestion of the antibody molecule; the Fab' fragments which can be generated by reducing the disulfide bridges of the $F(ab')_2$, fragment, the Fab fragments which can be generated by treating the antibody molecule with papain and a reducing agent.

In the production of antibodies, screening for the desired antibody can be accomplished by techniques known in the art, e.g. ELISA (enzyme-linked immunosorbent assay). For example, to select antibodies which recognize a specific domain of a PREB protein, one may assay generated hybridomas for a product which binds to a PREB fragment containing such domain. For selection of an antibody that specifically binds a first PREB homolog but which does not specifically bind a different PREB homolog, one can select on the basis of positive binding to the first PREB homolog and a lack of binding to the second PREB homolog.

5.2 DIAGNOSTIC METHODS

The present invention provides for a method of diagnosing the presence of an astrocytoma brain tumor in a subject as opposed to neuroepithelioma or glioma brain tumor, whereby the presence, amount, and/or molecular characteristics of the *PREB* gene, its corresponding mRNA or a cDNA thereof, or its gene product are determined. The presence of *PREB* RNA transcripts or protein would indicate the presence of astrocytoma brain tumor cells but not neuroepithelioma or glioma brain tumor cells and would possibly determine a course of treatment for the subject. Also included within the scope of the invention is the diagnosis of astrocytoma metastasis to the spinal fluid of the subject by the presence of *PREB* RNA transcripts or protein. As the metastatic potential of a malignant tumor may correlate with its presence in spinal fluid, a determination of the level of *PREB* mRNA or protein expression in a spinal fluid sample may have prognostic value, where high levels may bear a positive correlation with increased metastatic potential. The present invention also provides for a method of diagnosing trisomy 2p whereby the presence, amount, and/or characteristics of the *PREB* gene, its corresponding mRNA or a cDNA thereof, or its gene product are determined. Additional copies of the region of chromosome 2p encoding for PREB would indicate the trisomy 2p condition. The trisomy 2p condition is characterized by a syndromic phenotype that includes facial dysmorhism, mental and growth retardation, skeletal defects of the trunk and limbs and abnormalities of the genitalia. *See* Lurie et al., *Am. J. Med. Genet.* 55:229-236 (1995); Winsor et al., *Prenatal Diagnosis* 17:665-669 (1997).

In addition to being linked with trisomy 2p, the 2p23 chromosome region has also been significantly linked with hereditary low-bone mineral density, an identifying trait of osteoporosis. *See* Devoto et al., *Eur. J. Hum. Genet.* 6:151 (1998); Niu et al., *Hum. Genet.* 104:226 (1999). Subjects with familial osteoporosis contain homozygous deletions incorporating all, or nearly all of the *PREB* gene (*see* Example 14 and Figure 17). Subjects with familial osteoporosis or subjects having general propensity for developing osteoporosis may also contain homozygous or heterozygous deletions incorporating part or all of the *PREB* gene. The administration of the *PREB* gene and/or its products to a subject with familial osteoporosis or a subject having a

propensity for developing osteoporosis can correct or prevent bone mass loss in said subject.

Accordingly, the present invention provides a method for detecting a propensity to develop osteoporosis in a subject comprising detecting a deletion of all or part of the *PREB* gene. A deletion may be detected using portions of the *PREB* gene sequence as primers and using the Polymerase Chain Reaction to determine whether the full length *PREB* gene is present. A shorter product than expected would indicate a deletion, and no product could indicate a total deletion. Alternatively, primers could be made which flank the *PREB* gene, so that a total deletion in the *PREB* gene may still produce a signal. A deletion may also be detected by using the *PREB* gene as a probe for hybridization. If the *PREB* gene is deleted in full or nearly in full, no signal will be produced. If the *PREB* gene is partially deleted, a band of a smaller size than expected for the full length would be detected. In addition, subjects having a propensity to develop osteoporosis may also have nucleotide variations, substitutions, disruptions of the *PREB* open reading frame, removal of regulatory regions of the *PREB* gene by chromosomal rearrangements or intro/exon shuffling/splicing defects.

In addition, the present invention provides a method for correcting or preventing bone mass loss in a subject comprising administering to said subject the *PREB* gene or its products. The *PREB* gene can be administered to a subject via a viral or non-viral vector comprising a nucleic acid encoding PREB by techniques known in the art. For example, the *PREB* gene may be contained in a plasmid, an adenoviral vector, an AAV vector, a retroviral vector or in a liposome. Alternatively, the PREB protein may be administered directly to a subject by techniques known in the art. Administration of PREB for the control or prevention of bone mass loss is useful where the loss of bone mass is correlated with a change in the *PREB* gene and gene products.

In specific, nonlimiting examples, the presence of *PREB* RNA transcript or protein in a subject may be evaluated by analyzing the RNA of the subject. In a specific, nonlimiting example, a sample of RNA obtained from the subject may be prepared, denatured, annealed with oligo(dT), and subjected to first

strand synthesis in the presence of reverse transcriptase to generate cDNA from the subject's RNA sample. Using specific primers for the *PREB* gene, (*e.g.* but not limited to, a primer corresponding to positions 1081-1097, SEQ ID NO:4 or 1776-1761, SEQ ID NO:5 and a primer corresponding to positions 1300-1318, SEQ ID NO:6 or 1654 -1636, SEQ ID NO:7, as shown in Figure 1B, SEQ ID NO:1, or a primer corresponding to SEQ ID NO:14 and SEQ ID NO:15, or any primers designed from the *PREB* gene, including the Human *PREB* gene), nested PCR may be employed to detect the presence of *PREB* mRNA. In addition, methods such as, but not limited to, SSCP, entire gene sequencing or any methods known in the art which can detect nucleotide variations in either genomic DNA or cDNA from a subject.

Similarly, in a nonlimiting embodiment of the invention, the expression of *PREB* RNA in a subject may be evaluated in a cell or tissue sample, for example, by using Northern blot analysis, wherein RNA prepared from the sample is electrophoretically separated in the presence of formamide, transferred to a membrane (e.g. nitrocellulose), baked, prehybridized, and then hybridized to a ^{32}[P]-labeled *PREB* probe for 15 hours, and autoradiographed to detect the presence of *PREB* RNA. In humans, three transcript sizes of the *PREB* mRNA are found corresponding to 2.2, 1.9, and 1.5 kilobases (as determined by a commercial Northern blot (Clonetech)). Alternatively, *in situ* hybridization techniques, RT-PCR, microarray technology and other methods known in the art which can identify and quantify PREB transcripts may be used to identify *PREB* RNA transcripts in cells and tissue sections.

Further, the expression of PREB protein in a subject may be evaluated. The PREB protein in a cell or tissue sample of a subject may be determined, for example, by Western blot analysis, wherein protein prepared from the sample is electrophoretically separated (e.g., in a polyacrylamide gel), transferred to a membrane (e.g., nitrocellulose) and then bound to anti-PREB antibody, which is either itself detectably labeled, or which is detected by a labeled secondary antibody.

The human *PREB* nucleic acid sequences of the present invention may also be useful in diagnostic methods to detect trisomy 2p. The presence of additional copies of *PREB* can be detected by Southern blot analysis or flourescent *in situ* hybridization (FISH) using nucleic acids corresponding to SEQ ID NO:1, SEQ ID

NO:12, or SEQ ID NO:16, and fragments thereof, including SED ID NO:13 or SEQ ID NO:15.

5.3 MODEL SYSTEMS

The present invention provides for non-human animal model systems and *in vitro* cell systems which may be used to evaluate the effects of increasing, decreasing, or altering the temporal expression pattern of PREB expression and may be used to evaluate the effects of modified *PREB* nucleic acid sequences which encode for mutant PREB protein and/or fusion proteins containing PREB. Such animals, or cells grown in culture, may carry, as a transgene, an exogenously introduced *PREB* gene or a *PREB* cDNA, in some or all of their cells.

In specific, nonlimiting embodiments of the invention, a PREB encoding nucleic acid molecule, as described above, may be exogenously introduced into a non-human animal or a cell line. The PREB-encoding nucleic acid molecule may be operatively linked to a promoter , which may be a *PREB* promoter, a promoter selectively active in target cells, or an inducible promoter (such as the metallothionine or tetracycline promoter) or a promoter which directs widespread or ubiquitous expression (such as a human cytomegalovirus promoter or a retroviral LTR promoter).

Transgenic animals carrying an exogenous PREB-encoding nucleic acid molecule may be produced by standard techniques, including, but not limited to, techniques described in United States Patent No. 4,736,866, PCT publication WO82/04443 and PCT publication WO88/00239. Such animals may also be produced by infection with vectors carrying a PREB encoding nucleic acid molecule in expressible form, or by inoculation with naked PREB-encoding DNA. Animals in which the endogenous *PREB* gene or its control elements have been altered by homologous recombination may be produced using techniques as set forth in United States Patent No. 5,464,764 or Bradley, 1991, *Current Op. Biotechnol.* 2:823-829. The present invention also contemplates animals in which one or more endogenous gene has been "knocked out" and an exogenous *PREB* gene or cDNA has been introduced.

Cell lines carrying an exogenous PREB-encoding nucleic acid molecule may be produced by standard techniques, including, but not limited to, techniques described in *Current Protocols in Molecular Biology*, 1998, John Wiley and Sons, Publishers. Such cell lines may also be produced by infection with vectors carrying a PREB encoding nucleic acid molecule in expressible form, or by transfection with a naked PREB-encoding nucleic acid. Cell lines in which the endogenous *PREB* gene or its control elements have been altered by homologous recombination may be produced using techniques as set forth in *Current Protocols in Molecular Biology*, 1998, John Wiley and Sons, Publishers. The present invention also contemplates cell lines in which one or more endogenous gene has been "knocked out" and an exogenous *PREB* gene or cDNA has been introduced.

Non-limiting examples of animals which may serve as non-human animal model systems include mice, rats, rabbits, chickens, sheep, goats, cows, pigs, and non-human primates.

Non-limiting examples of cell lines which may serve as model systems include cell lines which do not express PREB (*e.g.* C6 rat glial cells or the human equivalent glial cell line e.g. DBTRG-O5MG).

For example, non-human animals, or human and non-human cell lines, may be produced in which extra copies of the *PREB* gene or cDNA have been introduced, or a *PREB* gene under a strong promoter has been created or introduced into the animal, or cell lines, such that the level of PREB protein, or mutant PREB protein, in the animal, or in a subset of cells of the animal, or in cell lines, has been increased relative to normal levels. Preferably the increase is by at least 25 percent. Such animals, or cell lines, may be used to study the effects of increased PREB levels, or to study the effect of the introduction of a mutant PREB protein, or a PREB protein made as a fusion with another protein so as to inhibit Pit-1 transcriptional activity and prolactin expression as described above. Such model systems are useful in studying the effects of *PREB* on the development of non-human animals and for studying osteoporosis.

Alternatively, non-human animals, or human and non-human cell lines may be produced which have lower than normal levels of PREB expression in some

or all cells, by virtue of a defect introduced in one or more alleles of the endogenous *PREB* gene and/or its control elements. For example, but not by way of limitation, one or both alleles of the endogenous *PREB* gene in the animal, or cell line, may be eliminated or mutated by gene targeting techniques. Alternatively, an additional *PREB* gene with altered structure may be introduced which competes with endogenous PREB and thereby inhibits native PREB activity. The effects of PREB on bone mass may be studied in such model systems.

In other nonlimiting examples, non-human animals which have been engineered to have autoimmune disease (*e.g.* arthritis, diabetes, lupus), osteoporosis, a reproductive disorder, or AIDS related syndromes, such as, but not limited to, those animal model systems described in U.S. Patents 5,777,193, 5,718,883, 5,489,742, 5,530,179, 5,675,060; 5,663,482 and 5,489,742, may be produced to over-express PREB either by the introduction of extra copies of the *PREB* gene or cDNA or engineered by the introduction of a *PREB* gene under a strong promoter. Such animals may be used to study the effect of increased prolactin levels on non-human animals with autoimmune disease, osteoporosis, a reproductive disorder or AIDS.

In other specific nonlimiting examples a PREB-encoding nucleic acid molecule of the invention, which has been mutated such that it can bind to the 1P element of the Pit-1 promoter, but cannot transactivate, may be introduced into a transgenic non-human animal which has a propensity for developing cancer (*e.g.* animal model systems described in U.S. Patents 5,777,193, 5,811,634, 5,709,844, 5,698,764, and 5,550,316). Because the mutated PREB would be expected to compete with endogenous PREB for 1P binding, such an animal may be used as a model system to study the effect on the development of cancer after a reduction in the expression of the prolactin gene.

In further nonlimiting examples, transgenic non-human animals may be produced in which a mutated *PREB* gene which cannot transactivate but can bind the 1P element of the PRL promoter and/or which contains other nucleic acid sequences forming a fusion protein which cannot transactivate but can bind the 1P element of the PRL promoter and block Pit-1 binding, and such mutant *PREB* genes may be over-expressed by the introduction of multiple copies of the gene or by the use of a strong

promoter, as discussed above. Such animals may be used as a model system to study the effects of the levels of serum prolactin on the development and control of graft-versus-host disease where transplantations (*e.g.* skin grafts, kidney, heart, liver, brain tissue, etc) are performed on the animal. Within the scope of the invention, is the same study where there are increased levels of PREB, creating a model system for studying the propensity for graft-versus-host disease in subjects with increased serum prolactin.

5.4 PREB AND OSTEOPOROSIS PROPENSITY

Osteoporosis is a skeletal disease characterized by low bone mineral density and microarchitectural deterioration of the bone structure, which leads to impaired skeletal strength and increased susceptibility to fracture (Consensus Development Conference, 1993). Bone mineral density (BMD), determined by dual energy x-ray absorptiometery (DEXA), is currently used to determine the risk of fracture.

Women over 50 years of age are at the greatest risk for developing osteoporosis (Melton et al., *J. Bone Miner. Res.* 7:1005 (1992)), which is thought to arise from the loss of estrogen post menopause (Riggs et al., *J. Bone Miner. Res.* 13:763 (1998)). Other well known risk factors include diet, premature or surgical menopause, late onset or irregular menstruation, extended lactation and endocrinopathies, such as hyperprolactinemia and gondal dysgenesis. Previous studies have shown that individuals with a family history of bone fracture are twice as likely to suffer fractures than the general population, and it has been suggested that genetic factors account for 70-80% of all variance in bone phenotype. For these reasons, much recent research has focused on the identification of genes and allelic variants predisposing, or conferring susceptibility to osteoporosis, with the majority of studies analyzing BMD measurements as the determining factor. Although, for example, allelic variations in the vitamin D receptor, the estrogen receptor, TGF beta receptor, interleukin 4 and 6, apolipoprotein E, collagen types 1a1 and 1a2, and the PTH receptors, have all been reported in association with reduced BMD, much further work is necessary to elucidate the genetic complexity of osteoporosis (reviewed in

Eisman J.A. 1999).

While genome-wide scans for loci with linkage to BMD have recently been performed (Niu et al., *Hum. Genet.* 104:226 (1999)). Linkage analysis on seven families previously reported with a recurrence of low spine and hip BMD has been previously performed. Loci on chromosome 11q, 1p36, and chromosome 4qter were identified. The region 2p23-24 was also found to have significant linkage with both low hip and spine BMD. A more recent study using families of Asian origin showed evidence of linkage with distal forearm BMD to chromosome 13q34, and both proximal and distal forearm BMD to two individual loci on chromosome 2 (2p21.1-p21.3 and 2p23-p24) (Niu et al., *Hum. Genet.* 104:226 (1999)).

The human PREB gene has been mapped to a region on chromosome 2p23 previously linked to low bone mineral density (BMD) (Figure 17 and Example 14). Low BMD is the most common risk factor for developing osteoporosis, a disease that has been associated with abnormal hormone levels, as well as defects in bone growth and remodeling processes. Chromosome 2p23 has also been associated with a trisomy syndrome manifesting various skeletal abnormalities. Therefore, disruption of the PREB gene will result in low BMD, leading to osteoporosis.

This invention has shown the existence of allelic variations of the PREB gene in one nuclear family within a large pedigree exhibiting BMD linkage to the PREB locus. Two children within this family, both of whom manifest low spine and hip BMD, were homozygously deleted for exons 2-9 of the PREB gene (containing nine exons in total) (*see* Example 14 and Figure 17).

The role for PREB in osteoporosis can be determined by an investigation of the biochemical function of this protein, involving an analysis of the molecular pathways in cellular development and differentiation that PREB protein may interact with and/or regulate. The yeast-two hybrid system to can identify proteins, particularly expressed at murine embryonic day 14.5 in murine embryonic stem (ES) cells, that interact with PREB.

Stable murine ES cell lines containing targeted mutations of the Preb gene can be generated. These lines can be differentiated *in vitro* into mature cell lineages. DNA microarray technology can also be employed to investigate gene

expression in cells of skeletal lineages expressing abnormal levels of the Preb gene transcript. A mouse model can then be generated with a targeted disruption of the Preb gene since murine models have been shown to be very powerful in elucidating the role of genes in both development and the mature organism.

The rat PREB protein of the present invention is a novel transcription factor, that exhibits binding to the prolactin promoter, and can upregulate prolactin and growth hormone gene expression in vitro (Fliss et al., *Mol. Endocrinol.* 13:644 (1999)).

Analysis of the expression of the human PREB gene of the present invention has shown that PREB is ubiquitously expressed in both adult (Fliss et al., 1999), and fetal tissue (Clelland et al., *Genomics,* In Press, incorporated herein by reference). However, the expression level differs among tissues, with the highest levels detected in adult salivary gland, liver, pancreas and skeletal muscle, and fetal liver (Clelland et al., *Genomics,* In Press, incorporated herein by reference). Analysis of Preb gene expression during murine embryogenesis detected transcripts in the perichondrial region of all major subdivisions of the fetal skeleton. In early staged embryos this corresponds to mesenchyme cells located in the future cervical region and thus the first branchial arch and immediately adjacent caudal tissue; while at later stages expression is detected in Meckel's cartilage, the basicranium, the developing rib shafts and the long bones of the forelimbs and hindlimbs. The most extensive expression of Preb is observed in the perichondrium of the craniofacial, axial and appendicular skeleton. Preb transcripts are also observed in the inferior wall of the genital tubercle, and the precursor of the developing pituitary gland. The PREB gene is highly conserved in mammals and invertebrates. Analysis of Drosophila melanogaster *Preb* gene expression shows the presence of transcripts in the salivary gland of early embryos (Clelland and Lo, in preparation).

The murine *Preb* gene of the present invention has been mapped to proximal chromosome 5 (Clelland et al, *Genomics*, In Press), and to the syntenic region on human chromosome 2p23. This region has been commonly associated with a chromosome re-arrangement syndrome known as Trisomy 2p syndrome. Although variable, the common duplication phenotype includes facial abnormalities, skeletal

defects, growth and mental retardation, congenital heart and neural tube defects, and abnormalities of the genitalia. The skeletal abnormalities commonly include dolichostenomelia (long tapering fingers and fan-like position of the toes), polydactyly, and long bone abnormalities. Deformities of the rib cage and vertebrae, and delayed bone age have also been reported. Abnormal dosage of the PREB gene may result in some of the abnormalities observed in this syndrome.

PREB gene expression is important during skeletal development. Murine *Preb* is co-expressed with genes in the perichondrium of the developing skeleton, known to function in the feedback signaling pathways controlling chrondrocyte differentiation and osteoblast formation. The abnormal dosage of PREB may result in skeletal abnormalities, and the mapping of human PREB to a region linked to low BMD, are all consistent with the hypothesis that PREB may function in both bone development and adult bone re-modeling. The role for PREB in the recurrence of low BMD in families with linkage to chromosome 2p23-24, can be analyzed as well as the biochemical role of PREB in cells of skeletal lineages.

The *PREB* gene has been mapped to chromosome 2p23-24 and an EST clone of the PREB gene has been made that has been positioned on the radiation hybrid map (WICGR) at position 158.27cR from the top of the chromosome 2 linkage group. This locus falls within the YAC contig WC2.2 (Whitehead Institute) to which the marker D2S170 has also been mapped. Consistent with this mapping data, the PREB EST has also been mapped to the NCBI GeneMap, between the markers D2S165-D2S352 (~5cM distance), which overlaps distally with the area of linkage within the low BMD pedigree.

An allelic variation of the PREB gene segregates in members of the family with low BMD. This was shown with primers designed to amplify the entire PREB gene in each individual, including all intron/exon boundaries, for direct sequence analysis. PCR experiments of one nuclear family, in which the mother and two children had low hip and spine BMD yielded no amplification of the PREB gene downstream of exon 1 in either of the two children, although flanking sequences on chromosome 2p23 did amplify, along with experimental control genes that map to chromosome 12 and 4. This result strongly suggests the presence in these two

individuals, of a homozygous deletion of the PREB gene downstream of exon 1.

Exon 1 of the PREB gene PCR amplifies when using a primer pair designed from sequence within this exon. Amplification is totally lost when the primers map within intron 1, suggesting that, at least for one chromosome, a breakpoint of this deletion maps within intron 1. This data is consistent with the a small, microscopic, interstitial deletion. Analysis of the microscopic deletion can be carried out by Southern blot hybridization to determine dosage of the PREB gene, using DNA isolated from each individual in the nuclear family and all other members of the large pedigree. The Southern analysis can be used to search for abnormal restriction enzyme patterns within the genomic region including and flanking PREB. Restriction patterns can be compared to genomic sequence of the region. Using the results of sequence data obtained above, primers can be designed for PCR amplification to amplify across the deletion boundaries on both chromosomes in each individual. Cloning and sequence analysis of all deletions can thus be achieved.

G-banding and FISH analysis (using the two genomic PACs that incorporate the PREB gene), on metaphase chromosomes (derived from lympoblastoid cell lines of blood) from each individual in the nuclear family can also be performed to determine whether large structural rearrangements occur in the *PREB* gene. This information can be used to design PCR primers that flank large deletions to identify deletion boundaries. Cloning and sequencing of large deletions can be performed by PCR, using the Expand long PCR system (Boehringer Mannheim) for large product amplification.

Northern analysis of human PREB transcript size, using the full length rat cDNA as a hybridization probe, has identified three possible alternatively spliced PREB transcripts of sizes 2.2kb, 1.9kb, and 1.5kb in the six human adult tissues examined (Fliss et al., 1999). Although the pattern of transcripts is tissue specific, the 2.2kb PREB transcript was expressed in all tissues examined. The 1.9kb transcript from a human cDNA library derived from a embryonic lung fibroblast cell line, M42 has been obtained. This transcript (SEQ ID NO:16; Figure 15A) arises from alternative splicing of the PREB gene primary transcript, yielding an mRNA in which exon seven is deleted, and a frameshift occurs (*see* Figure 16 and SEQ ID NO:18 for a

complete genomic sequence representation of the human *PREB* gene). The resultant encoded protein loses 84 amino acids from the C-terminus of PREB, and has an additional 17 novel residues at this terminus, followed by a stop codon (SEQ ID NO:17. Figure 15B).

In situ hybridization has demonstrated that murine Preb is expressed in the perichondrium of the developing bone (Taylor Clelland et al., 2000), and it is mesenchyme cells within this distinct element that differentiate into osteoblasts. The PREB protein isoforms involved in bone development and remodeling can be determined by analyzing which murine and human transcripts are expressed in particular skeletal lineages.

The yeast-two hybrid system involves an experimental procedure that, with new advances in vector technology, yeast strains, and the addition of interaction reporter genes, has become a reliable technique to look for interactions between proteins. Using the MatchMaker system, version 3 (Clontech, Palo Alto, CA), to minimize the number of false positives, both the 417 amino acid, and 350 amino acid PREB isoforms described above have been cloned into a GAL4/binding domain vector, and expressed in the yeast strain AH109. This transformed strain can be used in a co-transformation with a murine embryonic day 14.5/GAL4 activation fused cDNA library. Interacting clones can be sequenced, and the interaction with PREB confirmed by experiments involving GST pull-down assays, and or immunoprecipitation assays using a PREB antibody. The identification of PREB-interaction proteins, expressed during murine development can provide information regarding both upstream and downstream molecular pathways in which PREB plays a role. An example of the use of this system to characterize a WD-motif protein and provide evidence that the protein has a major role in a human development syndrome has been previously reported (Magnaghi et al., 1997).

Mouse embryonic stem cells (ES), derived from the inner cell mass of the early blastocyst, are used for the generation of genetically altered mice. Furthermore, studies have been performed which utilize the ability of totipotent ES cells to differentiate into lineages derived from each of the primary germ layers, following induction with specific growth stimuli (Keller, 1995). This ES cell property

has resulted in their use as an in vitro model to characterize developmental gene expression at the cellular and molecular level. Stable ES cell lines that are either homozygously or heterozygously deleted for Preb, or trisomic for the Preb gene can be generated using these techniques. These lines can be generated using the loxP/cre recombinase gene targeting system. A murine 129/SvevTACfBr whole genomic PAC library (HGMP) has been screened and eleven PACs that hybridize to the murine Preb have been isolated. The intron/exon boundaries of Preb can be determined from these PACs and the sequence data can be used to design a construct for homologous recombination with an ES cell strain compatible with the PAC genomic sequence (as described in Lindsay et al., 1999).

The ES cell lines can be induced to differentiate into mature osteoblasts, employing BMP-2 as the growth stimulant (Katagiri et al., 2000), through an intermediate differentiation into myoblast cells using conditions described previously (Rohwedel et al., 1994). At each stage of differentiation, cell types can be characterized by RT-PCR analysis of known tissue specific transcripts. Microarray technology can then be employed to examine simultaneously the expression levels of thousands of murine genes in response to an abnormal dosage of the PREB gene. Following probe hybridization, expression levels of transcripts can be analyzed. This approach can determine molecular pathways involving Preb gene expression.

The overall physiological role(s) of PREB can be determined using the stable ES cell lines described above to generate a mouse with a targeted disruption of Preb which can be used as a model system to study osteoporosis and BMD.

5.5 REGULATION OF PROLACTIN EXPRESSION AND TREATMENT OF DISEASE

The present invention provides for methods of treating cancer, autoimmune disease, developmental defects, reproductive disorders and osteoporosis through the regulation of prolactin expression via the alteration of *PREB* gene products, mutants, fusions and derivatives thereof or through the regulation of PREB itself.

In certain embodiments of the invention, the cancer, autoimmune disease, developmental defects, reproductive disorders or osteoporosis is associated with elevated levels of prolactin expression, in which case it is desirable to decrease PREB transactivation activity and/ or Pit-1 transactivation activity accordingly to reduce prolactin expression in a subject or in a particular tissue or cell population of the subject. Such a decrease in PREB expression may be achieved by either inhibiting the expression of the endogenous *PREB* gene, for example, by the administration of an antisense RNA or ribozyme or an inhibitor of the *PREB* promoter, or inhibiting the action of PREB protein, for example, by over-expressing a transactivation-negative-DNA-binding-positive mutant of a PREB fusion protein which may also be capable of inhibiting Pit-1 transactivation activity (as described above) or by administering an anti-PREB antibody (or a fragment or derivative thereof) which is capable of inhibiting the PREB transactivation activity and/or its DNA binding activity. Conditions which may benefit from such treatment include, but are not limited to, breast cancer, ovarian cancer, prostate cancer, pituitary tumors (where the inhibition of the expression of PRL may inhibit or reduce tumor growth), rheumatoid arthritis, systemic lupus erythematosus, autoimmune type I diabetes, adjuvant-induced arthritis, collagen type II-induced arthritis (where reduced serum levels of prolactin may favorably influence the prognosis of the disease), and graft-versus-host disease (where reduced serum levels of PRL may eliminate the host reaction to the transplanted graft). As PREB may also be a ubiquitous transcription factor, defects in PREB alone may result in adverse conditions. In such a case, it is desirable to control the levels of PREB to effectuate a down-regulation or up-regulation of transcription generally.

Similarly, cellular proliferation may be inhibited by a decrease in PREB expression which may be achieved by either inhibiting the expression of endogenous *PREB* genes as described above (i.e. by the administration of *PREB* antisense RNA, over-expression of a PREB inhibitor protein, or over-expression of a transactivation-negative-DNA-binding-positive PREB mutant).

In other embodiments of the invention, the cancer, autoimmune disease, developmental defect, reproductive disorder or osteoporosis is associated with decreased levels of prolactin expression, in which case it is desirable to increase

PREB transactivation activity accordingly in a subject or in a particular tissue or cell population of the subject. Such an increase may be achieved by the over-expression of PREB protein in a manner that stimulates prolactin expression either through the introduction of multiple copies of the *PREB* gene or cDNA, and/or through the introduction of a *PREB* gene or cDNA operatively linked to a strong promoter. Conditions which may benefit from such treatment include, but are not limited to, AIDS, immunosuppression, and some cancers. Additionally, where over-expression of TGF-beta is implicated in disease development, over-expression of PRL may overcome the undesirable effects of TGF-beta.

In particular embodiments, the present invention provides for a method of increasing PRL expression in a tissue of a subject in need of such treatment, comprising increasing the amount of PREB transactivation activity in the tissue using methods as set forth above. Nonlimiting examples of such tissues include tissues of the immune system, bone marrow, and skin.

In alternative embodiments, the present invention provides for a method of decreasing the expression of prolactin in a tissue of a subject in need of such treatment, comprising decreasing the amount of PREB activity in the tissue using methods as set forth above. In a specific nonlimiting embodiment, the tissue is a breast carcinoma, prolactinoma, or prostate carcinoma.

Administration of the foregoing agents may be local or systemic, using a suitable pharmaceutical carrier. Other compounds which aid in the uptake or stability of these agents, or which have beneficial pharmaceutical activity, may also be included in the formulations of the invention.

5.6 EXPRESSION OF FOREIGN GENES

The present invention provides for methods for the expression of exogenous genes, *in vivo* or *in vitro,* comprising the administration of a polycistronic vector which may incorporate a *PREB* gene (or a corresponding cDNA or RNA) as part of a polycistronic expression cassette together with a second gene, or multiple genes (or corresponding cDNA or RNA) whereby the second gene (or multiple genes), is operably linked to the 1P element of the PRL promoter and hence transactivated by

PREB. The *PREB* gene (or a corresponding cDNA or RNA) may be operatively linked to a constitutive promoter or an inducible promoter (*e.g.* the constitutive major intermediate early promoter of cytomegalovirus or the metallothionine promoter). Also within the scope of the invention, are multiple vectors whereby the *PREB* gene (or corresponding cDNA or RNA) is incorporated into a vector and whereby another vector contains other heterologous genes operably linked to the 1P element of the PRL promoter.

In certain embodiments of the invention, in the vector described above, the second gene may encode for a growth factor, or multiple growth factors (*e.g.* of growth factors; Epidermal Growth Factor (EGF), Fibroblast Growth Factor (FGF), Platelet Derived Growth Factor (PDGF), Nerve Growth Factor (NGF)) and may be introduced into skin cells, brain cells, immune cells (B-cell hybridomas), or bone marrow cells grown *in vitro* in order to stimulate the growth of such cells which could ultimately be transplanted to a subject but is not limited to the enumerated cells. Such cells could be used therapeutically to treat burns or other wounds, Alzheimer's disease, Parkinson's disease, AIDS, or leukemia. Additionally, such cells may be autologous to the intended host.

In other, nonlimiting embodiments of the invention, the vector described above may be administered to a subject *in vivo* to result in its introduction into skin cells, bone marrow cells, brain cells, immune cells. Such a vector may stimulate the growth of the subject's cells.

In further, nonlimiting embodiments of the invention, the vector described above may stimulate the growth of primary cell lines *in vitro* which otherwise would divide a finite number of times in culture. Such cell lines may be useful for long term studies of primary cell lines.

In alternative, nonlimiting embodiments of the invention, in the polycistronic vector described above, the second gene may encode for a heterologous protein or peptide. Such a vector may be stably transfected into an immortalized eukaryotic cell line which lacks endogenous PREB expression (*e.g.* a cell line with a "knock-out" mutation of the endogenous *PREB* gene) to result in the enhanced expression of the heterologous gene of interest for subsequent *in vitro* studies and/or

for mass production. In such embodiments, the *PREB* gene may be optionally operably linked to an inducible promoter.

In related embodiments rather than a single vector comprising *PREB* and a second gene of interest, a first vector comprising *PREB* operably linked to a first promoter element, and a second vector comprising the second gene of interest operably linked to a second promoter which comprises a 1P element, may both be introduced into an immortalized eukaryotic cell line.

It is noted hereby that certain results described in the working Examples below regarding the role of PREB in PRL expression have been inconsistent.

6. EXAMPLE: IDENTIFICATION OF THE PREB CODING SEQUENCE

6.1. MATERIALS AND METHODS

"Southwestern" screening. A filter-bound, denatured-renatured expression library was screened with a concatenated probe as described in Singh et al., 1988, *Cell* 52:415-423 and Vinson et al., 1988, *Genes Dev.* 2:801-806.

[^{32}P]-labeling of DNA. Prolactin promoter element 1P DNA was [^{32}P]-labeled as described in *Current Protocols in Molecular Biology*, John Wiley and Sons, publishers (1996).

Preparation of cDNA library. A bacteriophage cDNA library was prepared from the GC rat pituitary cell line as described in Bancroft, 1981, *Functionally Differentiated Cell Lines* 47-59 Alan R. Liss, New York, publishers.

6.2 RESULTS

To search for factors that might play a role in regulation of prolactin gene expression via the proximal Pit-1 DNA binding site 1P, this DNA element was employed as a probe to screen a bacteriophage cDNA library prepared from the GC rat pituitary cell line λZAPII cDNA library (Stratagene, La Jolla, CA.). Screening of 1.5 x 10^6 plaques yielded several presumptive positive clones that bound to labeled site 1P. However, only one of these clones exhibited DNA-sequence specificity: binding

to element 1P, but not to either a mutated element 1P or a canonical CRE. The properties of this clone, designated PREB, were further investigated. The pBLUESCRIPT vector containing *PREB* cDNA was excised *in vivo*, and the cloned cDNA was sequenced, yielding a 1.28 kilobase sequence containing a large (240 amino acid) open reading frame, but lacking a putative initiator methionine. Successive applications of 5'-RACE (rapid amplification of DNA ends) of GH3 cell RNA yielded an additional 636 bases, resulting in the *PREB* cDNA sequence shown in Figure 1B (SEQ ID NO:1), containing in-frame methionine codons at positions 1 and 217. The ATG at position 217 is preceded by ACC, matching well the Kozak consensus (SEQ ID NO:8), while the ATG at base 1 is preceded by the poorly matching sequence GGG (SEQ ID NO:9). The sequence following each methionine encodes PREB containing, respectively, either 345 amino acids (~38kD) or 417 amino acids (~46kD). Putative polyadenylation and AU-rich mRNA shortened half-life elements in the cDNA 3'UT were also noted.

7. EXAMPLE: SEQUENCE SPECIFIC BINDING TO THE 1P ELEMENT

7.1. MATERIALS AND METHODS

Electrophoretic mobility shift assay. Partially purified recombinant his-tagged PREB (PREB amino acids 175-417, preceded by six histidines) was prepared from transformed *E. coli* by solubilization of an insoluble pellet in binding buffer (5 mm imidizole, 0.8 M NaCl, 10 mM Tris {pH 7.9}, 8 M urea), application to a nickel affinity column, gradual refolding on the column by progressive dilution of the urea (as described in Vinson et al., 1988, *Genes Dev.* 2:801-806), elution in buffer containing 0.5-1.0 M imidizole, followed by desalting and concentration in an Amicon (Beverly, MA) spin column. Double-stranded oligonucleotides corresponding to prolactin promoter sites 1P, *1P, 1P*, and 3P, (Figure 3C) and the CLE have been previously described in Yan et al., 1991, *Mol. Endocrinol.* 5:535-54 and Yan et al., 1994, *Mol. Cell Endocrinol.* 101:R25-R30. The sequence of the double-stranded SP1 binding site oligonucleotide probe (containing a 5' Sal In site) is 5'-TCGACGGGGCGGGGCC-3' (SEQ ID NO:10), and of the double-stranded rat GH pGHF-1 site is

5'-TCGACTGGCTCCAGCCATGAATAAATGTATAGGGAAAG-3' (SEQ ID NO:11). All procedures were performed at 4°C in the presence of protease inhibitors (1 mM PMSF, 1 μg/ml aprotinin, and 5 μg/ml leupeptin). The partially purified his-tagged PREB was then incubated 10 minutes at room temperature in 9 μl containing 10 mM Tris (pH 7.9), 60 mM KCL, 1 mM EDTA, 0.03% NP40, 4% Ficoll, 1 mM DTT, 5 μg poly(dI-dC), 1 μg BSA, with or without unlabeled DNA competitors, then an additional 10 minutes following addition of 1 ng ^{32}P-end-labeled site 1P probe, followed by analysis on a 5% polyacrylamide gel in .25x TBE at 4°C. The dried gel was then autoradiographed 1-3 hours at -70°C with intensifying screens.

Imaging of gels. Autoradiograms of gel blots or photographs of gels were recorded electronically using an AGFA (ARCUS II) Scanner (Leverkusen, Germany).

7.2. RESULTS

PREB exhibits DNA sequence-specific binding to prolactin promoter element 1P. Electrophoretic mobility shift was employed to examine the DNA sequence binding specificity of recombinant PREB (Figure 3A). PREB plus the element 1P probe that was employed to clone PREB yielded a single shifted band (lane 2), which was competed by excess cold element 1P (lanes 3-5). Use of element 1P mutants (illustrated in Figure 3B) showed that PREB binding to element 1P was also inhibited by an excess of the 1P* mutant (lanes 9-11), but not the *1P mutant (lanes 6-8). The inability of *1P to compete implied that the PREB site in element 1P is located at least partially on the 5' side of this element (Figure 3C). Since X-ray analysis has recently shown that the Pit-1 POU domain binds to element 1P as a dimer by contacting the bases bracketed in Figure 3B as described in Jacobson et al., 1997, *Genes Dev.* 11:198-212, the ability of 1P* to compete PREB binding implied that Pit-1 and PREB possess different, but possibly overlapping, binding sites within element 1P. The observation (Figure 3A) that PREB binding was not competed by excess amounts of oligonucleotides corresponding either to the Pit-1 binding site, PRL-3P (lanes 12-14) or GH-GHF1 (lanes 15-17), or to two unrelated DNA sequences, an SP1 binding site (lanes 18-20) or the PRL promoter CLE sequence as described in

Coleman et al., 1996, *Endocrinology* 137:1276-1285 (lanes 21-23), further confirmed the DNA binding specificity of PREB. Since no known DNA-binding motif can be detected in the PREB amino acid sequence shown in Figure 1B (SEQ ID NO:2), this specificity is likely to be conferred by a novel DNA-binding motif. These results are consistent with the use of the 1P element as the promoter sequence for any gene which can then be expressed by the co-expression of PREB.

8. EXAMPLE: PREB IS A SINGLE COPY GENE AND IS REVOLUTIONARILY CONSERVED

8.1. MATERIALS AND METHODS

Southern Blot Analysis. Restriction enzyme-digested DNA was transferred to nitrocellulose filters according to the Basic Protocol described in Ausubel et al. *(Short Protocols in Molecular Biology*, Third Edition, 1995, John Wiley and Sons, Publisher), Unit 2.9 A. Prehybridization and hybridization were then performed at 39° C according to the Basic Protocol described in *Short Protocols in Molecular Biology*, Unit 2.10 (Appendix 1), employing a ^{32}P random-primed rat PREB cDNA probe and the aqueous prehybridization/hybridization (APH) solution. Filters were washed as described in *Short Protocols in Molecular Biology*, Unit 2.10, including the two optional 15 minute moderate-stringency washes described (42° C; 0.2x SSC/0.1% SDS).

8.2. RESULTS

Southern blot analysis was employed to determine the structure and number of *PREB* genes in various organisms (Figure 4 A-D). Digestion of rat DNA with the DNA restriction enzymes EcoRI and HindIII, XhoI and PvuI yielded, respectively single or double bands on an agarose gel. The double bands detected with the latter two enzymes probably correspond to cleavage with an intron, since the *PREB* cDNA sequence contains neither recognition site. Single bands were detected upon digestion of human DNA with any of four enzymes (Figure 4B). Thus *PREB* is apparently a single copy gene that is well-conserved between rat and human (Figure 4A and Figure 4B respectively). Restriction enzyme digestion of either Drosophila or

Yeast DNA also yielded one or two bands that hybridized with rat *Preb* cDNA, implying that the *PREB* gene (or a related gene) has been highly conserved during evolution (Figure 4C and Figure 4D). The ability of rat *Preb* to hybridize to the DNA of other organisms was the basis for the determination that the gene is well conserved among various species.

9. EXAMPLE: PREB CAN FUNCTION AS A TRANSCRIPTIONAL ACTIVATOR

9.1. MATERIALS AND METHODS

Preparation of anti-PREB antiserum. Inclusion bodies were prepared from *E. coli* expressing recombinant his-tagged PREB (PREB amino acids 175-417, preceded by six histidines), (as described by Sambrook et al., 1989, *Molecular Cloning: A Laboratory Manual*. Cold Spring Harbor Press, Cold Spring Harbor, publishers). Cells were lysed with lysozyme and deoxycholic acid in the presence of 50 mM PMSF, treated with DNAse (1 mg/ml) at room temperature for 15 to 30 minutes, and subjected to centrifugation. The pellet was then suspended, washed with 6.5 M urea in 0.1 mM Tris, pH 8.5, then PREB was extracted with elution buffer (8 M urea, 50 mM Tris, pH 8.0, 1 mM EDTA, 100 mM NaCl, 0.1 mM PMSF), and subjected to SDS-PAGE gel electrophoresis. A gel fragment containing the major PREB band was excised, frozen, ground with a mortar and pestle, and supplied frozen to Cocalico Biologicals, Inc. (Reamstown, PA.) for preparation of antiserum in rabbits according to their standard protocol. Prior to use in Western Blot analysis and immunocytochemistry, either anti-PREB antiserum or preimmune serum from the same animal was preadsorbed with extracts of host *E. coli*. An equal volume of 2X SDS sample buffer was added to a pelleted 50 ml bacterial culture, mixed thoroughly, incubated at 65-70°C for 10 minutes, fractionated on a 4.5% SDS-PAGE mini-gel employing a 1.5 mm preparative comb, and transferred to nitrocellulose. After soaking the filter in a 5% solution of Carnation brand non-fat milk, the filter was incubated on a rocking platform either one hour at room temperature or 4°C overnight, with anti-PREB antiserum diluted 1:250 into TBST buffer (20 mM Tris, pH 7.6; 137 mM NaCl, 0.1% Tween-20) containing 3% bovine serum albumin, and the adsorbed antiserum employed for analysis of PREB.

Western blot analysis. Nuclei and cytosol (i.e. the soluble fraction of the post-nuclear supernatant) were prepared from GH3 cells as described by Lee et al. *Gene Anal. Tech.* 5:22-31 (1988), in the presence of the protease cocktail containing 1 mM PMSF, 1 μg/ml aprotinin, and 5 μg/ml leupeptin. Preliminary SDS-PAGE electrophoresis analysis revealed no gross degradation of proteins in either fraction, and that on a per cell basis, the cytosol contained a considerably higher protein content than the nucleus. Samples were subjected to SDS-PAGE, transferred to nitrocellulose on a semi-dry transfer apparatus (Hoeffer Scientific Instruments, San Francisco. CA), employing Towbin buffer (25 mM Tris, 192 mM glycine, 0.0372% SDS, 20% methanol) for 30 to 60 minutes at 100 mAmps. Filters were blocked for 1 hour with 5% Carnation non-fat dry milk in TBST, incubated with anti-PREB antibody (1:250), followed by washing with TBST. The filter was then exposed to secondary antibody (conjugated to horseradish peroxidase and diluted 1:5000) in TBST containing 3% bovine serum albumin for 30 to 60 minutes. Following washing with TBST (4 times 10 minutes), immunoreactive proteins were visualized by enhanced chemiluminescence according to the directions of the manufacturer (Amersham Corporation, Arlington Heights, IL).

Immunocytochemistry of Cultured Cells. Cells were plated on glass cover slips in serum containing media the night before use (C6 cells, DMEM plus 5% fetal calf serum; GH3 cells in Ham's F10 plus 15% horse serum plus 2.5% fetal calf serum). For use with GH3 cells, the cover slips were first coated with CellTak (14 μg/25 mm cover slip) (Collaborative Biomedical Products, Bedford, MA). The cells were washed twice with phosphate buffered saline (PBS), fixed 20 minutes at room temperature in 2% paraformaldehyde, incubated 20 minutes in blocking buffer (0.6% Tween 20 in DMEM containing 5% fetal calf serum) and then incubated overnight at 4°C with either 1:250 dilutions of preimmune serum or anti-PREB, each preadsorbed as described above. The dishes were then washed three times with PBS, and incubated 30 minutes with rhodamine-labeled goat anti-rabbit IgG (American Qualex, LaMiranda, CA) at 1:500 in blocking buffer, rinsed three times, and mounted in Mowiol. Images were captured using a 40X oil objective on a Nikon inverted microscope with a Cohu CCD4910 camera in conjunction with a Colorado video

integrator unit. Digital data were processed with Metamorph software from Universal Imaging, Media, PA.

Transient co-transfection assays. For each treatment group, approximately $0.5x10^8$ or $2x10^6$ C6 cells were subjected to electroporation. Preliminary experiments were performed with PRL-CAT constructs and a known prolactin promoter regulator, Pit-1, to optimize transfection efficiency for each cell line. For transfection, cells were resuspended in 0.75 ml DMEM containing 10% fetal bovine serum plus the indicated plasmids, and subjected to electroporation at 960 μF and either 300 volts (C6 cells) or 240 volts (GH3 cells), divided among three 60 mm tissue culture dishes, and incubated 48 hours as described above for each cell line. One day following transfection, each dish was examined microscopically, and any experiment that exhibited gross differences in cell survival among different treatment groups was discarded. Cells were then harvested with a rubber policeman, lysed by sonication (2 minutes x 4) in 0.25 M Tris, pH 7.8, 10 mM EDTA, and heated to 65°C for 10 minutes to inactivate deacetylases. Half of each cell extract was assayed for CAT activity as described previously (Fischberg et al. Mol. Endocrinol. 8:1566-1573. 1994), employing [^{3}H]chloramphenicol (0.01 μCi/μl) and butyryl CoA (5 mg/ml) and a 4 hour incubation, which yielded results in the linear range of the assay. The remainder of the cell extract was employed for assay of β-galactosidase activity as described (Ausubel et al., 1996 *Current Protocols in Molecular Biology*. John Wiley and Sons, publishers). For each experimental condition, the average CAT assay result was divided by the average β-galactosidase activity under that condition, relative to a value of 1 assigned to the average β-galactosidase activity in the controls. It may be noted that this procedure always yielded a correction of ≤2%. Each experiment reported here has been repeated a total of at least three times, with results similar to those shown in the figures.

Plasmids. The construction of plasmids (-1957) PRL-CAT and (-113) PRL-CAT was described previously. Jackson et al. Mol. Endocrinol. 2:1139-1144 1988 and Lufkin et al. Science 237:283-286 1987. RSV-PKA was prepared by employing PCR primers to amplify the murine PKA catalytic subunit described in Uhler et al. *J. Biol. Chem.* 262:15202-15207 (1987), followed by Hind III/Xba In

restriction endonuclease digestion of the amplified product, and ligation into the corresponding site in plasmid RcRSV (InVitrogen). RSV-Pit-1 (Fox et al., 1990, *Mol. Endocrinol.* 4:1069-1080.) and RSV-β-gal were kindly supplied by Dr. H. Samuels (New York University). GAL4 constructs pSG424 (Sadowski et al, 1989,. *Nucleic. Acids. Res.* 17:7539 referred to in the present paper as pGAL4(1-147)) and 5XGAL4-CAT (Carey et al., 1990, *Nature* 345:361-364) were kindly supplied by Dr. M. Ptashne (Sloan-Kettering Institute). GAL4-PREB was constructed by cloning the PREB coding sequence (amino acids 1-417) upstream of and in register with the GAL4(1-147) sequence in pSG424. RSV-PREB was constructed by cloning the PREB coding sequence into the HindIII/XbaI site of RcRSV.

9.2. RESULTS

PREB can function as a transcriptional activator. To determine whether PREB might serve as a pituitary cell transcription factor, the expression and intracellular location of PREB protein in the GH3 rat pituitary cells was investigated. Nuclear or cytosolic proteins isolated from an equal number of cells were subjected to Western blot analysis (Figure 5A). Anti-PREB antiserum, but not control preimmune serum, detected a major 45 kD band that accumulates preferentially in nuclei. This observation implies that PREB is a nuclear protein in pituitary cells. In addition, the size of the protein detected suggests both that synthesis of this protein was initiated by the more N-terminal methionine encoded by the *PREB* cDNA sequence (i.e., amino acid 1 in Figure 1B; SEQ ID NO:2) and that the entire *PREB* cDNA coding sequence had been cloned.

The intracellular location of PREB was examined further by immunocytochemical analysis (Figure 5B-D). With anti-PREB antiserum, the pituitary GH3 cells yielded a strong signal that was located specifically over the nuclei (Figure 5B), while control rat glial C6 cells yielded only a faint diffuse background signal (Figure 5D). Preimmune serum also yielded only a background signal with either cell line (Figure 5C). The observation that PREB cross-reacting material exhibited a substantial nuclear accumulation in pituitary cells was consistent with a role for PREB as a cellular transcription factor.

To investigate directly the possible role for PREB as a PRL gene transcription factor, the ability of this protein to transactivate prolactin promoter activity in rat glial C6 cells was examined. The ability of PREB to regulate expression of a construct, (-1957)PRL-CAT, that contains the first 1957 base pairs upstream of the prolactin gene body, and thus covers both the promoter and enhancer regions (Nelson et al., 1988, *Science* 239:1400-1405) was first investigated. As expected from previous studies (Yan et al., 1994, *Mol. Cell. Endocrinol.* 101:R25-R30), this PRL-CAT construct alone was inactive in the C6 cells, but was activated by co-expression of Pit-1 (Figure 6). Co-expression of PREB was also observed to activate (-1957)PRL-CAT expression, showing that this protein exhibited equivalent activation of (-1957)PRL-CAT expression (Figure 6). This result demonstrated that PREB can transactivate PRL promoter/enhancer activity. This region of the PRL regulatory region contains at least seven Pit-1 binding sites. Nelson et al., 1988, *Science* 239:1400-1405. The similar levels of activity observed for Pit-1 and PREB on this construct thus suggested that the PRL promoter/enhancer region may contain multiple functional PREB binding sites.

Since element 1P is the only presently known PREB site in the PRL promoter (Figure 3B), this site was utilized in further functional studies of PREB. In order to study element 1P in its natural context within the PRL promoter, the ability of exogenously expressed PREB to trans-regulate construct (-113)PRL-CAT was investigated. As illustrated in Figure 7A, the only known prolactin promoter elements in this construct are the CRE-like element (CLE), element 1P, and a TATA box. The observation that the CLE did not bind PREB (Figure 3) implied that any effects of PREB (and/or Pit-1) on this PRL-CAT construct were mediated via element 1P. These results are consistent with the expression of heterologous genes which are operably linked to the 1P element of the PRL promoter by the over-expression of PREB.

A comparison of the abilities of various inputs of RSV-based vectors for Pit-1 and PREB to trans-regulate (-113)PRL-CAT (Figure 7A) expression yielded equivalent stimulation by the two proteins (Figure 7B). This result again demonstrates that PREB can act as a transcriptional activator of a PRL promoter

regulatory element. Furthermore, since Pit-1 is known to be a powerful transactivator of PRL gene expression (Fox et al., 1990, *Mol. Endocrinol.* 4:1069-1080; and Mangalam et al., 1989, *Genes Dev.* 3:946-958) , the observation of equivalent activities for Pit-1 and PREB on two prolactin regulatory region constructs (see Figure 6 and Figure 7B) implied that PREB can strongly regulated expression of this gene.

PREB and Pit-1 transactivation activity of prolactin gene expression are additive. The results of electrophoretic shift mobility analysis described above implied that the PREB and Pit-1 binding sites within element 1P are centered over different regions. We thus investigated the ability of PREB to regulate PRL promoter activity in the presence of Pit-1 (Figure 8). As before, transfection of equal amounts (2.5 μg) of an expression construct for either protein alone yielded transactivation of (-113)PRL-CAT. Co-transfection of 2.5 μg of expression vectors for each protein yielded a level of transactivation that was approximately additive over that yielded by either expression vector alone, suggesting that these two proteins exert additive actions on element 1P. Doubling the input of each expression vector, to close to maximal activity levels (see Figure 8), increased expression three-fold, again consistent with an approximately additive action of PREB and Pit-1. These observations suggested that, at least in the basal cellular state, these two proteins may exert actions on element 1P that are of approximately equal strength, but largely independent. This coupled with the DNA binding data suggested that the PREB and Pit-1 occupy proximal sites on the PRL promoter and is consistent with the ability of PREB fusion proteins to inhibit the binding of Pit-1 and block Pit-1 transactivation of PRL.

PREB can mediate transcriptional stimulation by PKA in either GH3 pituitary cells or heterologous C6 cells. As described above, previous studies have implied that Pit-1 is not the direct functional target of PKA action on the PRL promoter. Inspection of the predicted PREB amino acid sequence revealed a number of potential PKA phosphorylation sites. This, together with the observations described above that PREB can bind specifically to PRL element 1P and exhibited transcriptional activity, suggested that PREB may represent the cellular protein that directly mediates PKA action on the PRL promoter via element 1P. To begin to

investigate this possibility in GH3 cells, under conditions that are independent of both endogenous PREB and PREB binding sites, the ability of a GAL4-PREB to transmit PKA action to a co-transfected GAL4 indicator construct was investigated (Figure 9). As expected, control GAL(1-147) was unable to transactivate 5XGAL4-CAT expression, in either the presence or absence of an RSV-PKA expression vector. In the absence of RSV-PKA, GAL4-PREB alone strongly transactivated 5XGAL4-CAT, which demonstrated again that PREB contains a transcriptional activator domain. Co-transfection of RSV-PKA yielded a three-fold increase in the ability of GAL4-PREB to transactivate 5XGAL4-CAT. This observation demonstrated that PREB can support a PKA-mediated transcriptional response in pituitary cells, possibly in the absence of any change in its ability to bind DNA.

The ability of PREB to transmit a PKA transcriptional signal to the PRL promoter, in the absence of other pituitary cell signals was also investigated. To do this, the effect of expression of RSV-PKA in C6 glial cells on trans-activation by either Pit-1 or PREB of indicator construct (-113)PRL-CAT (Figure 10) was examined. As before, (-113)PRL-CAT alone exhibited minimal activity, which was only slightly increased by co-expression of PKA. Co-expression of Pit-1 strongly transactivated CAT activity. However, this activity was not further increased by co-expression of PKA, in agreement with previous observations (Okimura et al. Mol. Endocrinol. 8:1559-1565. 1994). In contrast, the trans-activation of CAT activity by PREB was strongly increased by co-expression of PKA. Thus, PREB (but not Pit-1) can support a PKA-mediated transcriptional response directed by element 1P in the context of the PRL promoter.

10. EXAMPLE: ISOLATION AND SEQUENCE ANALYSIS OF THE HUMAN *PREB* cDNA

10.1 MATERIALS AND METHODS

cDNA Library Screening, Sequence and Analysis. A Clontech (Palo Alto, CA) fetal brain cDNA library was plated and screened according to the manufacturer's instructions. All hybridization washes were performed in 1xSSC with 0.1%SDS at 65 °C. The cDNA inserts were isolated from positive phage clones

according to standard methods (*see* Chisholm, *Biotechs* 7:21-23 (1989), incorporated herein by reference), and subcloned into the plasmid pBS (Stratagene, La Jolla, CA) Double-stranded plasmid sequencing was performed using an ABI 377 sequencer (PE Bioscience, Foster City, CA) and PRISM Dye-terminators Cycle Sequencing Ready Reaction Kit (PE Bioscience, Foster City, CA), with FS enzyme kit (PE Bioscience, Foster City, CA). The primer ATGTCCTGGGTGCCGCGG (SEQ ID NO:14) was used to sequence across the 5' end of the open reading frame (ORF) in the 2.5 kb BamHI genomic pBS subclone. Both BamHI genomic subclones were sequenced entirely by primer walking, and all pBS clones were sequenced in both directions. cDNA sequence was translated using the GCG package (Human Genome Mapping Project (HGMP), Cambridge, UK).

PAC Library Screening. A human chromosome 2 specific PAC library was obtained from the Human Genome Mapping Project (HGMP) resource center (Cambridge, UK). A SacII-BamHI fragment of the rat *PREB* cDNA was labeled with ^{32}P-dCTP and hybridized overnight at 65 °C in a hybridization solution containing: 6x SSC, 0.3% SDS, 50 mM NaH2PO4 (pH6.2), 5x Denhart's solution and 50 µg/ml denatured salmon sperm. The filter was washed to a stringency of 1x SSC/0.1% SDS, at 65 °C, and exposed to x-ray film (Kodak, Rochester, NY). A PstI fragment, incorporating exon two of the murine *Sax2* cDNA, was labeled and hybridized to the genomic PAC filter as described above, except that washes were performed in 6xSCC/0.1% SDS solution, and an additional hybridization and wash at 42 °C was also performed. Each experimental condition was repeated using the *Sax2* probe after competition for one hour, at 65 °C, with human genomic DNA. Positive clones were requested and received from HGMP.

10.2 RESULTS

A SacII/BamHI fragment of rat *PREB* cDNA (which encompasses the entire open reading frame (ORF), was used to screen a human fetal brain cDNA library (Clontech, Palo Alto, CA). Two positive clones (FB6 and FB8) were identified, isolated and sequenced and found to be identical in size except for the absence from FB6 of 49 bases of the 5' sequence. The sequence of the 1.9 kb FB8

clone was shown to be >83% identical with the rat *PREB* cDNA over the entire length of the cDNA clone, including the 3' untranslated region (UTR). A long ORF, encoding 412 amino acids was observed in FB8, possessing > 89% identity and 91% similarity to rat PREB, implying that it encodes the human PREB homologue. However, comparison between the predicted human and rodent PREB proteins showed that five amino acid residues, including the initiating methionine residue, were absent from the human protein. In contrast, an ATG that encodes a second methionine residue, located downstream in both rat and mouse PREB transcripts, was conserved in the human transcript.

A primer was designed to determine the initiation site of human PREB translation which was used to sequence across the 5' end of the ORF in a 2.5 kb BamHI genomic fragment from a human PAC (14K14) that incorporates the *PREB* gene. Translation of the resultant nucleotide sequence predicted an additional five residues possessing 100% identity with the N-terminus of the rodent PREB proteins, including the initiating methionine. BESTFIT analysis (GCG at HGMP) showed a further sequence from PAC 14K14 with nucleotide homology to the 5' UTR of the cloned PREB transcripts, indicating a possible human 5' UTR of 144bp. This sequence data implies that FB8 represents a partial cDNA clone, and that the full length human PREB transcript encodes a protein of 417 residues in length. The sequence of the full length FB8 transcript, the predicted amino acid sequence including the amino acid residues (SEQ ID NO:13) predicted from the SEQ ID NO:12, and the 5' UTR are all shown in Figure 11A.

BLAST analysis showed that the PREB protein has significant sequence similarity with the yeast TUP1 transcriptional repressor protein (Genbank Accession Number p16649; Williams and Trumbly, *Mol. Cell. Biol.* 10:6500-11(1990) incorporated herein by reference), and Pfam database screening identified PREB as a WD-repeat family member. Three potential WD repeats are conserved among all PREB homologues characterized to date (*see* Figure 12). Figure 12 shows that the three WD-repeats in human PREB are conserved with rat and mouse PREB repeats 1, 2 and 3 respectively and with regions of the yeast TUP1 protein (accession number p16649; Williams and Trumby, *Mol. Cell. Biol.* 10:6500-6511 (1990). PREB

repeat 3, although highly similar to the WD consensus sequence, does not share amino acid sequence with any of the yeast TUP1 repeats, and instead is most similar to a WD-repeat within a hypothetical yeast protein (accession number p53877). The two proline-glutamine rich amino acid regions, which have been noted by Fliss et al., *Mol. Endocrinol.* 13:644-657 (1999), incorporated herein by reference, are also highly conserved among rat, mouse and human PREB proteins.

11. EXAMPLE: ANALYSIS OF *PREB* GENE EXPRESSION

11.1 MATERIALS AND METHODS

Northern Analysis. A human RNA master blot, containing standardized mRNA levels from 43 human adult and seven fetal tissues were hybridized and washed according to the manufacturer's instructions (Clontech, Palo Alto, CA). All *PREB* probes were prepared for hybridization to the RNA filter according to the manufacturer's instructions (Clonetech). A 55 bp fragment was PCR amplified from the PAC 14K14, using the following primers:

Forward: ATGTCCTGGGTGCCGCGG (SEQ ID NO:14);

Reverse: TGAAACGAGTACAACGGGA (SEQ ID NO:15).

Genomic DNA (100 ng) was denatured for 5 minutes and then subjected to 30 cycles of denaturing at 94 °C, annealing at 61 °C, and extension at 72 °C, each for 30 seconds.

11.2. RESULTS

Northern analysis showed the presence of a three possible alternatively spliced transcripts of 2.2 kb, 1.9 kb and 1.5 kb in six human adult tissues examined. Although these transcripts are apparently produced in tissue specific patterns, at least one *PREB* transcript was expressed in all tissues examined, with largest 2.2 kb transcript being present in every tissue.

A human RNA "master blot" (Clonetech) was hybridized to a 350 bp PstI fragment derived from the 3' UTR of the human transcript. Following stringent washing, *PREB* transcripts were detected in all 43 adult tissues and seven fetal tissues represented on the blot (*see* Figure 13A-D). The same filter was used in all

experiments, the signal being stripped and filters checked by autoradiography before each re-hybridization. Ubiquitin cDNA hybridization to the RNA filter was used as a control (Figure 13B). The filter was washed at 0.1xSSC/1% SDS at 50 °C, and exposed to x-ray for 16 hours. Before hybridization, the ^{32}P-labeled probe was denatured and then competed with human Cot-1 DNA for one hour at 68 °C, according to the manufacturer's instructions (Clontech). Although PREB was ubiquitously expressed (Figure 13C), after a 16 hour exposure to x-ray film, the levels of expression varied greatly among tissues; with very high levels detected in adult salivary gland, liver, pancreas and skeletal muscle, and fetal liver tissue. In Figure 13C, the hybridization and washing conditions, and probe preparation were identical to the control probe experiments. In contrast, the lowest levels of expression were notably in the adult aorta and lung (*see* Figure 13D). The expression patterns detected may be indicative of a major function in tissues exhibiting very high expression levels. The signal observed in H4 (13C and 13D) is due to the presence of contaminating *E.coli* DNA within the *PREB* clone DNA preparation from which the probe was made.

To investigate whether PREB transcripts extend further 5' than the sequence contained in the FB8 clone, and thus might contain the more upstream methionine codon identified previously in rat PREB (*see* Fliss et al, *Mol. Endocrinol.* 13:644-657 (1999)), PCR primers were designed to amplify a 55 bp fragment of the human *PREB* gene between the two putative methionine codons from the genomic PAC 14K14. The amplified product was ^{32}P-labeled and then hybridized to the RNA blot described above. The hybridization pattern in all tissues, including brain tissues, was identical to that described above using the 3' UTR region of *PREB* as a probe. This result suggests that the full length *PREB* transcript extends further than the FB6 and FB8 clones isolated from the fetal brain cDNA library, and that this predicted human transcript corresponds to the 2.2 kb *PREB* transcript.

The 1.9 kb FB8 cDNA may correspond to a *PREB* transcript splice variant described by Fliss et al, *Mol. Endocrinol.* 13:644-657 (1999). The FB8 transcript would encode an N-terminally truncated protein. Preliminary studies have identified two putative splice variants of a Drosophila cDNA that encode proteins

with high similarity to the mammalian PREB proteins. It is possible that the multiple bands observed (*see* Fliss et al, *Mol. Endocrinol.* 13:644-657 (1999)) arise from cross-hybridization between related mRNA transcripts. The 2.2 kb transcript would then represent the sole human *PREB* mRNA species.

12. FISH MAPPING TO HUMAN CHROMOSOME 2P23 AND GENOMIC ORGANIZATION OF THE *PREB* GENE

12.1 MATERIALS AND METHODS

FISH. Metaphase spreads were prepared from EBV-transformed cell lines and peripheral whole blood by standard techniques. *See* Barch et al., *The AGT Cytogenics Laboratory Manual,* Lippincott-Raven, New York (1997), incorporated herein by reference. Maxiprep PAC cDNA (prepared using Maxiprep, Qiagen, Valencia, CA, according to the manufacturer's instructions) was labeled by nick translation with Digoxigenin-11-dUTP (Boehringer Mannhein). *In situ* hybridization was carried out as follows: The hybridization mixture [150 ng probe DNA, 4 μg Cot-I DNA, and 7 μg Herring Sperm DNA (Gibco/BRL, Rockville, MD) in Hybrisol VII (Oncor, Gaithersburg, MD) was applied to heat denatured normal metaphase spreads and hybridized overnight in a humid chamber at 37 °C. Unbound DNA fragments were removed by washing in 2xSSC at 72 °C for 5 minutes and 1x PBD (phosphate buffered detergent) for 3 minutes at room temperature. Slides were then incubated with 60 μl anti-Digoxigenin rhodamine (Oncor), for 15 minutes at 37 °C. This was followed by three-3 minute washes in 1x PBD at room temperature. FISH images were captured with an ImagePoint cooled CCD video camera (Photometrics, Tuscan, AZ), through a Labophot-2A fluorescence microscope (Nikon, Melville, NY). Chromosome identification was facilitated by counterstaining with 0.1 μg/μl DAPI in Vectashield (Vector Latoratories, Burlingame, CA). *See* Florijn et al., *Cytometry* 19:177-182 (1995).

12.2 RESULTS

Preliminary somatic cell hybrid mapping, using a human oligo-dT primed EST (ATCC 125415, Manassa, VA) with homology to the 3' UTR of the rat *PREB* cDNA, localized the human gene to chromosome 2. A human chromosome 2

specific PAC library (HGMP) was screened with the SacII/BamHI rat *PREB* fragment described above, and two positive PACS were identified: 14K14, and 14I02. Each was used as a probe in FISH analysis of normal metaphase chromosome spreads and each yielded identical specific signals on human chromosome 2, within the G-band 2p23 (*see* Figure 14A and 14B).

The two *PREB* positive PACs described above were employed to investigate the genomic organization of the *PREB* gene. BamHI digestion of each PAC yielded two fragments, about 2.5 kb and 1.6 kb in size, that specifically hybridized to a probe of the full length human *PREB* transcript. These fragments were subcloned into the plasmid pBS and sequenced. The entire *PREB* gene was localized within these two BamHI fragments and shown to span 3.7 kb. *PREB* contains eight exons, varying in size between 81 bp and the largest 769 bp exon at the 3' end of the gene. All intronic 5' acceptor and 3' donor sites are consistent with consensus sequences.

The murine *Preb* gene has previously been mapped to proximal murine chromosome 5; a region sytenic to both human chromosome 4p16 and 2p23 (*see* Clelland et al, *Genomics*, In Press (2000), incorporated herein by reference). The murine *Sax2* gene, a member of the small group of homeobox genes related to the Drosophila *NK1* homoedomain (*see* Chen and Lufkin, *Mamm. Genome* 8:697-8 (1997), incorporated herein by reference), co-segregates with murine *Preb* in the progeny of a BSS2 specific backcross panel (Clelland, et al, *Genomics,* In Press (2000)). Although the human *Sax2* gene has not been cloned, the above results imply that a human homologue of this gene will map either to 4p16 or 2p23. Further in support of this, a 3.0 kb genomic fragment containing the entire homeodomain (exon 2), of the murine *Sax2* gene was hybridized to a human chromosome 2 specific library (HGMP), using varying hybridization and wash conditions as well as probe competition with human total genomic DNA. No positive genomic PAC clones were detected in any of the hybridization experiments, suggesting that the human *Sax2* gene will likely map to human chromosome 4p16.

13. MAPPING OF *PREB* WITHIN A REGION ASSOCIATED WITH HUMAN TRISOMY 2P SYNDROME

13.1. RESULTS

The FISH mapping described above localized the human *PREB* gene to a region associated with a partial trisomy syndrome in humans. Of the sixty cases reported of trisomy 2p, 43 encompass the chromosome band 2p23. *See* Clelland et al, *Genomics,* In Press (2000); Magarbane et al., *J. Med. Genet.* 34:783-786 (1997); Patel et al., *J. Med. Genet.* 34:949-951 (1997); Winsor et al., *Prenatal Diagnosis* 17:665-669 (1997); Al-Saffar et al, *Am. J. Med. Genet.* 87:45-48 (1999), all incorporated herein by reference. In over one third of these individuals, the proximal breakpoint within chromosome 2 maps to 2p23, which may be indicative of a repetitive region within this genomic DNA that pre-disposes to structural rearrangements, as observed elsewhere within the human genome. *See* Halford et al., *Hum. Mol. Genet.* 2:191-196 (1993); Phimister, *Nat. Genet.* 16:11 (1997); Small et al., *Nat. Genet.* 16:96-99 (1997), incorporated herein by reference. A role for *PREB* in the trisomy phenotype would imply that *PREB* maps to the commonly duplicated region of 2p23. The dosage of *PREB* was analyzed in the individuals described above. PAC 14K14 was hybridized to metaphase chromosome spreads and interphase nuclei obtained from the individuals with duplication breakpoints within 2p23 (11 and Coriell Cell repositories, Al-Saffar et al., *Am. J. Hum. Genet.* 65Supp(4):850 (1999), incorporated herein by reference), and two individuals whose region of duplication extends from 2p21-pter (Scola, *Am. J. Human. Genet.* 31:110A (1979); Lurie et al, *Am. J. Med. Genet.* 55:229-236 (1995), both incorporated herein by reference). In all four cases, three signals were detected in each interphase nuclei examined, and all metaphase chromosomes clearly showed the presence of three copies of the *PREB* gene (*see* Figure 14C, 14D, 14E, 14F, and 14G).

14. ROLE OF PREB IN OSTEOPOROSIS

Four human DNA samples were obtained from a nuclear family with the mother and two sons diagnosed with osteoporosis (supplied by Dr. Loretta Spotilla, Thomas Jefferson University, Philadelphia, PA) and analyzed for mutations

of the *PREB* gene. The DNA from the two sons contained large homozygous deletions, incorporating all, or nearly all of the *PREB* gene, suggesting a correlation between familial osteoporosis and mutations in the *PREB* gene. Initial experiments were performed to PCR amplify the entire human *PREB* gene, including intron and exon boundaries, using the following four primer pairs (which all map to intronic or untranslated sequence of the *PREB* gene):

Forward 1: CTCGGCTTCCTGCTGATGGT (SEQ ID NO:19)

Reverse 1: CAAGCGGGTCTTCCCAACA (SEQ ID NO:20)

Forward 2: CAGACTCTTCCCTAAACGTGCT)SEQ ID NO:21)

Reverse 2; ACTTACTGGGCAAGCAGCATA (SEQ ID NO:22)

Forward 3: CCCACGAAGGGGAGATTGAA (SEQ ID NO:23)

Reverse 3: GGGCACGTTTCTGGTCATTA (SEQ ID NO:24)

Forward 4: CTTTGAAGGGTTCTGGTTTTCA (SEQ ID NO:25)

Reverse 4 GGTCTCAGTTCACTCTTTCCTTGTTT (SEQ ID NO:26)

Denaturation was performed at 95°C for 1 min. Followed by an annealing step (specific temp for each primer pair; 1.5mM MgCl2 added and annealed at 52°C for Forward 1 and Reverse 1; 2.0mM MgCl2 / anneal 51°C for Forward 2 and Reverse 2; 2.5mM MgCl2 / anneal 50°C for Forward 3 and Reverse 3; and1.5mM MgCl2 / anneal 49°C for Forward 4 and Reverse 4)

for 1 min. Extension was carried out at 72°C for 1 min.

All PCRs were performed using commercial enzyme, buffers and dNTPs (Qiagen), and all PCR conditions were determined using control DNA.

One nuclear family was used for the initial experiment. The mother and one child have both low hip and spine bone mineral density (BMD), the second child has low hip BMD. The father is unaffected. The four PCR amplifications (using the primer pairs above) failed to amplify any products in either of the two children., however products were amplified in both parents and a control individual (Figure 17). To test the quality of DNA, primers were then designed to amplify the GAPDH pseudogene on chromosome 12, the osteopontin gene on chromosome 4, and the keteohexokinase gene that also maps to 2p23 (Figure 17). In all cases a product was obtained in each individual examined. Further primers were designed, in both

intronic and exonic sequences of the PREB gene, to ensure the failure of PCR amplification in the children was not due to experimental problems, such as shearing of genomic DNA, etc. In each case no amplifiable product was obtained (Figure 17), except when the primer pair CB306 (forward)/CB305 (reverse) (*see* primers below) were used. This primer pair amplifies a 105bp fragment in exon 1 of the PREB gene. However, in a further experiment using the primers CB306/Reverse 1, again no product was detectable.

CB306: ATGTCCTGGGTGCCGCGG (SEQ ID NO:27)

CB305: TGAAACGCGTACAACGGGA (SEQ ID NO:28)

(2.5mM MgCl2 / Anneal 52°C)

CB301: CAGCAGAGAAGAAATGTG (SEQ ID NO:29)

CB317: TGGTAGCGGTAAGGTGTGCTGG (SEQ ID NO:30)

(1.5mM MgCl2 / Anneal 53°C)

Various references are cited herein, the contents of which are hereby incorporated by reference in their entireties.

CLAIMS

1. A purified and isolated PREB-encoding nucleic acid molecule having the sequence set forth in Figure 1B (SEQ ID NO: 1).

2. The PREB-encoding nucleic acid molecule of claim 1, as contained in a vector molecule.

3. A purified and isolated PREB-encoding nucleic acid molecule having the sequence set forth in Figure 11A (SEQ ID NO: 12).

4. The PREB-encoding nucleic acid molecule of claim 3, as contained in a vector molecule.

5. A purified and isolated PREB-encoding nucleic acid molecule having the sequence set forth in Figure 15A (SEQ ID NO: 16).

6. A purified and isolated nucleic acid molecule which hybridizes to SEQ ID NO:1 under stringent conditions and which encodes a PREB protein capable of increasing expression of prolactin in a pituitary cell.

7. A purified and isolated nucleic acid molecule encoding a PREB protein, wherein the PREB protein has an amino acid sequence as set forth in Figure 1B (SEQ ID NO:2).

8. A purified and isolated nucleic acid molecule encoding a PREB protein, wherein the PREB protein has an amino acid sequence as set forth in Figure 11B (SEQ ID NO:13).

9. A purified and isolated nucleic acid molecule encoding a PREB protein, wherein the PREB protein has an amino acid sequence as set forth in Figure 15B (SEQ ID NO:17).

10. The nucleic acid molecule of claim 2, contained in an expression vector and operably linked to a promoter element.

11. The nucleic acid molecule of claim 10 contained in an expression vector c-terminal to another nucleic acid molecule which encodes for a domain protein thus forming a fusion protein.

12. The nucleic acid molecule of claim 10 wherein the promoter element is not the PREB promoter.

13. The nucleic acid molecule of claim 4, contained in an expression vector and operably linked to a promoter element.

14. The nucleic acid molecule of claim 13 contained in an expression vector c-terminal to another nucleic acid molecule which encodes for a domain protein thus forming a fusion protein.

15. The nucleic acid molecule of claim 13 wherein the promoter element is not the PREB promoter.

16. A purified and isolated nucleic acid molecule which comprises a primer for the *PREB* gene which may be used in a polymerase chain reaction having a nucleic acid sequence selected from the group consisting of:

a) SEQ ID NO:4;

b) SEQ ID NO:5;

c) SEQ ID NO:6;

d) SEQ ID NO:7;

e) SEQ ID NO:14; and

f) SEQ ID NO:15.

17. A method of inhibiting prolactin gene expression which comprises the over-expression of antisense mRNA of *PREB*.

18. A fusion protein which comprises a DNA-binding-competent, transcriptional-activation-defective PREB protein positioned c-terminal or n-terminal to the POU domain of Pit-1 protein.

19. A method of treating cancer which comprises administering to a patient a therapeutically effective amount of *PREB* antisense RNA.

20. A method of treating cancer which comprises administering to a patient a therapeutically effective amount of the fusion protein of claim 18.

21. A method of treating autoimmune disease which comprises administering to a patient a therapeutically effective amount of *PREB* antisense RNA.

22. A method of treating autoimmune disease which comprises administering to a patient a therapeutically effective amount of the fusion protein of claim 18.

23. A method for stimulating the proliferation of B cell hybridomas which comprises over-expressing the PREB protein.

24. A method of treating cancer in a subject comprising inhibiting the expression of prolactin in the subject using *PREB* antisense RNA.

25. A method of inhibiting the proliferation of a cell comprising inhibiting the expression of prolactin in the cell using *PREB* antisense RNA.

26. A method of treating a developmental defect in a subject which comprises administering to the subject a therapeutically effective amount of *PREB* antisense RNA.

27. A method of detecting trisomy 2p in a subject comprising (a) obtaining from said subject a DNA sample, (b) probing said DNA sample with a portion of the *PREB* gene, and (c) determining the presence of extra copies of the *PREB* gene therein.

28. A method of determining the propensity of a subject to develop osteoporosis comprising detecting a nucleic acid variation, including a deletion of all or part of a *PREB* gene in said subject, a variation in PREB mRNA and a variation in the genomic regulatory region, coding region and intronic regions of the *PREB* gene.

29. A method of determining the propensity of a subject to develop osteoporosis comprising detecting differential *PREB* gene transcript levels in said subject.

30. A method of treating osteoporosis in a subject comprising administering a nucleic acid encoding PREB to said subject.

31. The method according to Claim 29 wherein a vector comprises the nucleic acid encoding PREB.

32. The method according to Claim 30 wherein said vector is selected from the group consisting of a plasmid, an adenoviral vector, an AAV vector and a retroviral vector.

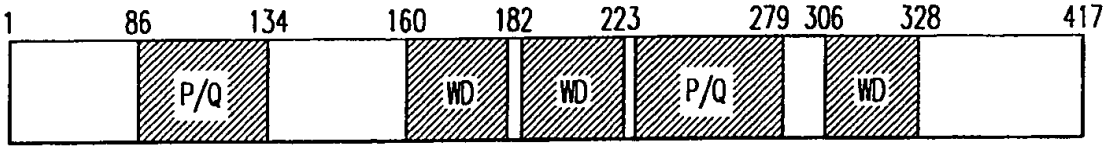


FIG. 1A

```
      -114 ccgagacccctcggcagtcttccggaaaactctagcgccaagttcctgagc
 tttcggaggcgaggcgcggcatgtcgtgggttccgcggggttggcggtgaacgtgcgggcggg

1     atgggtcggcgccgggggtgtggagctgtaccgggccccgttcccgttgtacgcgcttcgg
1     M  G  R  R  R  G  V  E  L  Y  R  A  P  F  P  L  Y  A  L  R
61    atagaccccaagactgggctgctcatcgctgcgggcggaggaggagctgccaagaccggc
21    I  D  P  K  T  G  L  L  I  A  A  G  G  G  G  A  A  K  T  G
121   ataaagaatggcgtgcatttttctgcagctagagctgatcaacgggtgcctgagcgcttcc
41    I  K  N  G  V  H  F  L  Q  L  E  L  I  N  G  C  L  S  A  S
181   ttgctgcactctcatgacacggagacacgggccaccatgaatttggcgcttgctggtgac
61    L  L  H  S  H  D  T  E  T  R  A  T  M  N  L  A  L  A  G  D
241   attcttgctgccggacaggatgcccagtgtcagcttcttcgtttccaggtccatcaacag
81    I  L  A  A  G  Q  D  A  Q  C  Q  L  L  R  F  Q  V  H  Q  Q
301   aagggcagtaaagcggagaagtcaggttccaaggagcacccaggtcgacagagaaagggg
101   K  G  S  K  A  E  K  S  G  S  K  E  H  P  G  R  Q  R  K  G
361   gctcctccagcagagaagaaatcgggagcacaagttcacccggaaggggttgaactcaaa
121   A  P  P  A  E  K  K  S  G  A  Q  V  H  P  E  G  V  E  L  K
421   gtaaagaatttggaggcagtacagacagacttcagcaatgaaccgctgcagaaagttgtg
141   V  K  N  L  E  A  V  Q  T  D  F  S  N  E  P  L  Q  K  V  V
481   tgcttcaaccatgataacaccctgcttgccaccggaggaactgatggtcatgttcgtgtc
161   C  F  N  H  D  N  T  L  L  A  T  G  G  T  D  G  H  V  R  V
541   tggaaggtacctagcctagagaaagttctggagtttaaagcccacgaaggggagattgga
181   W  K  V  P  S  L  E  K  V  L  E  F  K  A  H  E  G  E  I  G
601   gatttggctttgggtcctgatggcaagttggttactgtgggctgggactttaaggcctcc
201   D  L  A  L  G  P  D  G  K  L  V  T  V  G  W  D  F  K  A  S
661   gtgtggcagaaggatcaactggtgacacagctacagtggcaagagaatggacccacctct
221   V  W  Q  K  D  Q  L  V  T  Q  L  Q  W  Q  E  N  G  P  T  S
721   tctaacacaccgtaccgctaccaggcctgcaggtttgggcaggttccagatcagcctggt
241   S  N  T  P  Y  R  Y  Q  A  C  R  F  G  Q  V  P  D  Q  P  G
781   gggctgcgactcttcacagtgcagatacccccacaagcgcctacgacagccccccaccctgc
261   G  L  R  L  F  T  V  Q  I  P  H  K  R  L  R  Q  P  P  P  C
841   tacctcacagcctgggacagttccaccttcttgcctcttcggaccaggtcctgtggccat
281   Y  L  T  A  W  D  S  S  T  F  L  P  L  R  T  R  S  C  G  H
901   gaagtcatttcctgcctcactgtcagtgaatcgggtaccttcctaggcctaggcacggtc
301   E  V  I  S  C  L  T  V  S  E  S  G  T  F  L  G  L  G  T  V
961   actggctctgtcgccatctacatagctttctctctccagcgcctgtattatgtgaaggag
321   T  G  S  V  A  I  Y  I  A  F  S  L  Q  R  L  Y  Y  V  K  E
1021  gcccatggcattgtggtgacagatgtgaccttctacctgagaagggttgcggtccaaag
341   A  H  G  I  V  V  T  D  V  T  F  L  P  E  K  G  C  G  P  K
1081  ctccttgggccccatgaaacggccctgttctctgtggctgtggatagtcgttgccagttg
361   L  L  G  P  H  E  T  A  L  F  S  V  A  V  D  S  R  C  Q  L
1141  cacctgctgcctcacggcggagtgttcccgtatggctcctgctcctgctatgtgttggc
381   H  L  L  P  S  R  R  S  V  P  V  W  L  L  L  L  C  V  G
1201  cttattatcgtgaccatcctgctgctccagagtgccttcccgggggtttctttaacatcct
401   L  I  I  V  T  I  L  L  L  Q  S  A  F  P  G  F  L  *
```

FIG. 1B

1261 gaccaatgggagtcatccttggacagtactaccttctggagcagagtcattgaggcccat
1321 gactgaagctgcatctgatgaaatggatgggtactgccggtccctgctaaacgctgcgcc
1381 agtggcctccctatcactctgggtcttgggagccctgctttcacctgtggatccatttaa
1441 gacagtgtggtctgaagctcaggccacactgcctgcctcgtttcctctgcctcccagggc
1501 tccagagccgagctcttcctaggaacatgtgaagatgccaaagagcccagaggcattgcc
1561 atccttctcgcagagactgttttttcctcctcccctttccagtctgcgcacaaggtcctcag
1621 ctttgtcgagacaaagtctgtggaagaggcaaaaggaagacccaggtagcggtgatctgt
1681 aggtagcacccagccagtcaggccagacgcacagggagttcctgggtgacctactgcagc
1741 ctgaggaaagggaaagtgaacctcagtttattaggcaggaagagttgatatttAATAAAg
1801 aaaga

FIG.1C

```
  1 agatggctac gtccgtgtct ggaagggtgcc cagcctgtag aaggttctgg agttcaaagc
 61 ccacgaaggg aggattgaag acctggcttt agggcctgat ggcaagttgg taaccgtggg
121 ccgggacctt aaggcctctg tgtggcagaa ggatcagctg gtgacacagc tgcactggca
181 agaaaatgga cccacctttt ccagcacacc ttaccgctac cagggcctgc aggttttggc
241 aggttccaga ccagnctgct ggccttgcga cttttacag tgcaaatttt cccacaagc
```

FIG.2

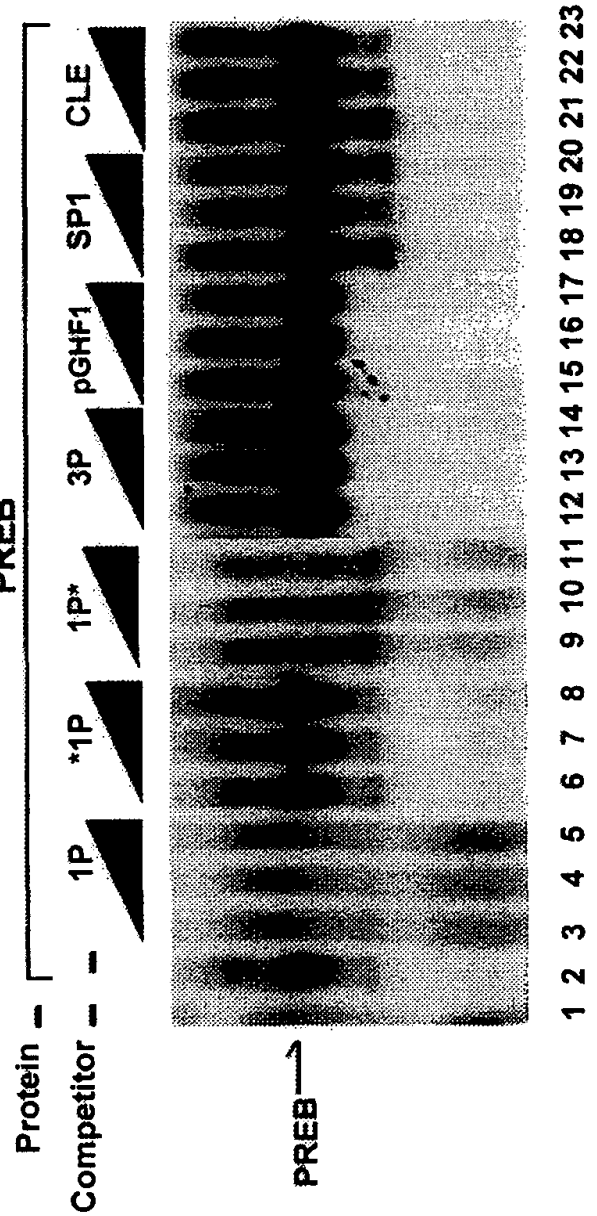

PREB
Protein
Competitor
1P
*1P
1P*
3P
pGHF1
SP1
CLE
PREB
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23

FIG.3A

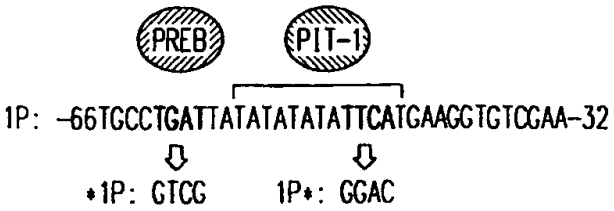

PREB
PIT-1
1P: -66TGCCTGATTATATATATATTCATGAAGGTGTCGAA-32
*1P: GTCG
1P*: GGAC

FIG. 3B

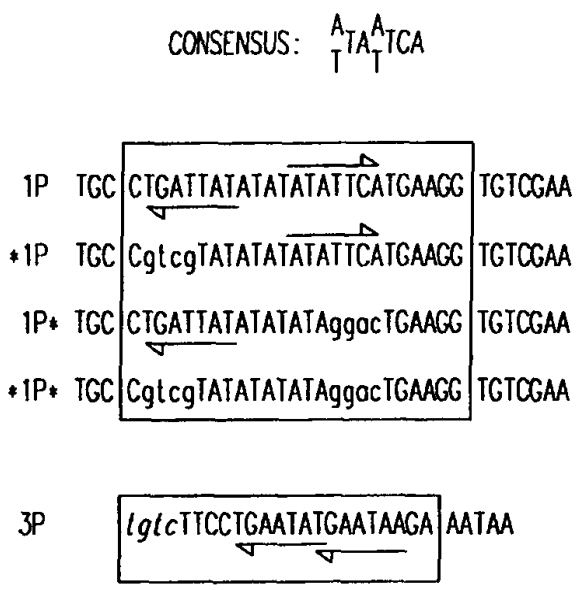
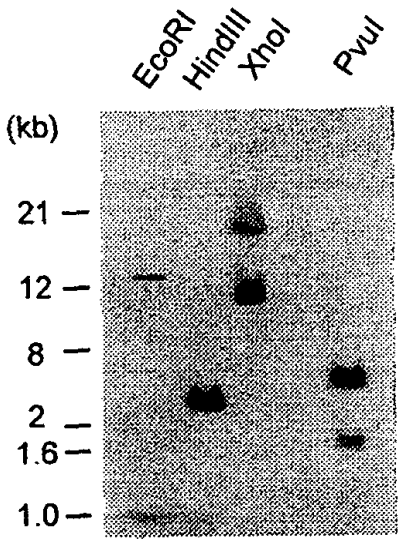
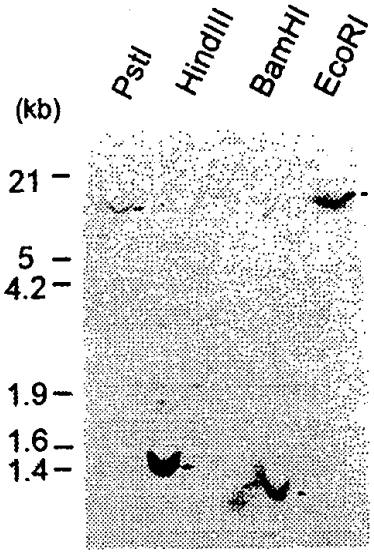

CONSENSUS: A/T TA A/T TCA
1P TGC CTGATTATATATATATTCATGAAGG TGTCGAA
*1P TGC CgtcgTATATATATATTCATGAAGG TGTCGAA
1P* TGC CTGATTATATATATAggacTGAAGG TGTCGAA
1P TGC CgtcgTATATATATAggacTGAAGG TGTCGAA
3P lgtcTTCCTGAATATGAATAAGA AATAA

FIG. 3C



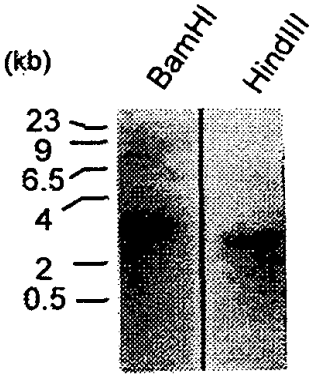
GH3 (rat)

FIG.4A



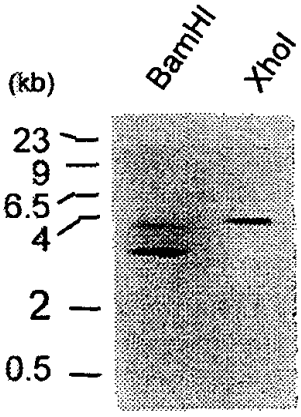
Human

FIG.4B



Drosophila

FIG.4C



Yeast

FIG.4D

FIG.5A

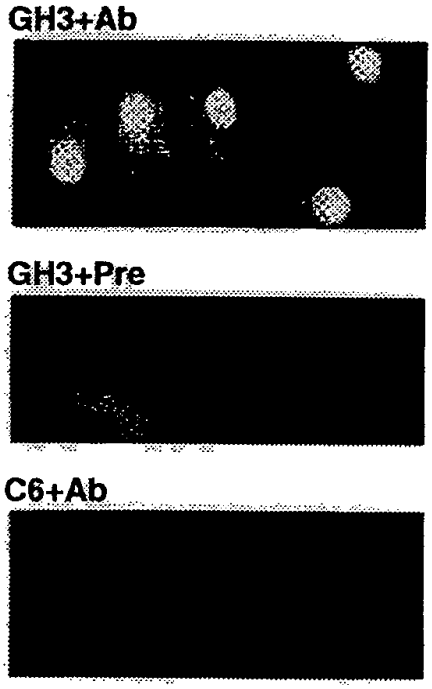


FIG.5B

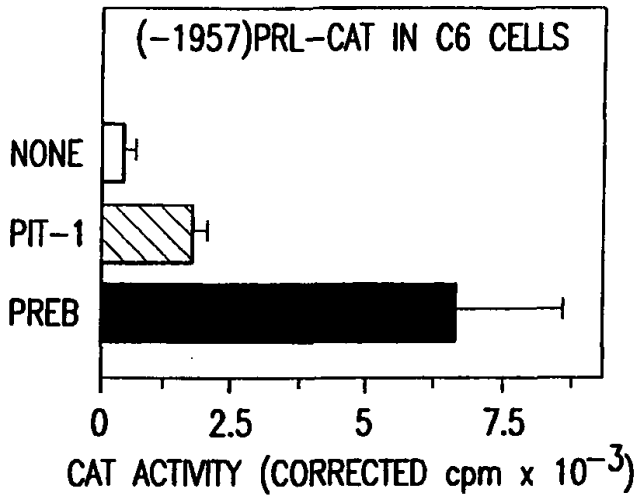


FIG.6

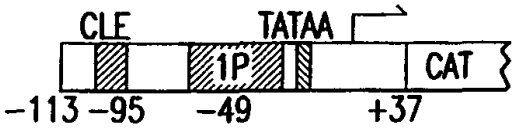


FIG. 7A

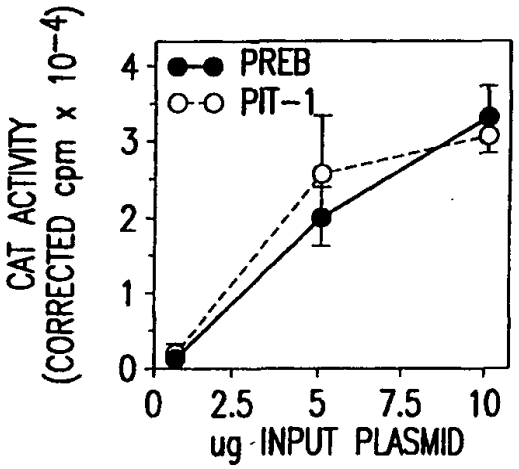


FIG. 7B

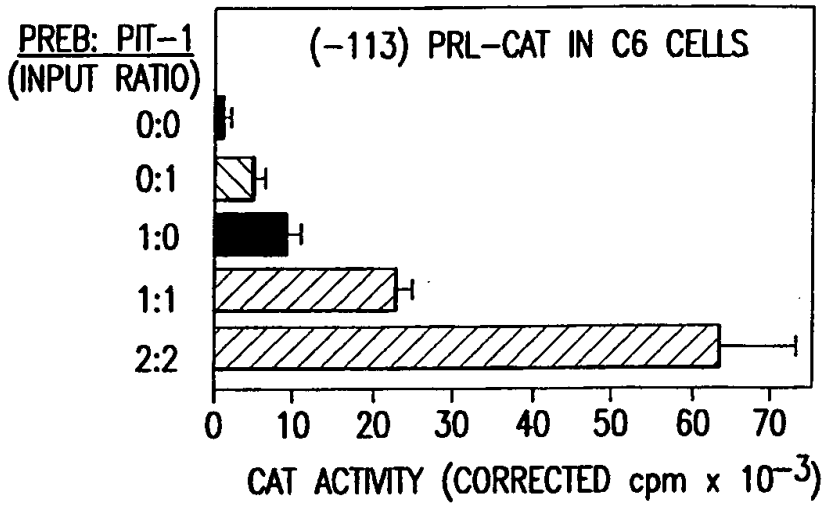

PREB: PIT-1
(INPUT RATIO)
(-113) PRL-CAT IN C6 CELLS
0:0
0:1
1:0
1:1
2:2
0
10
20
30
40
50
60
70
CAT ACTIVITY (CORRECTED cpm x 10-3)

FIG.8

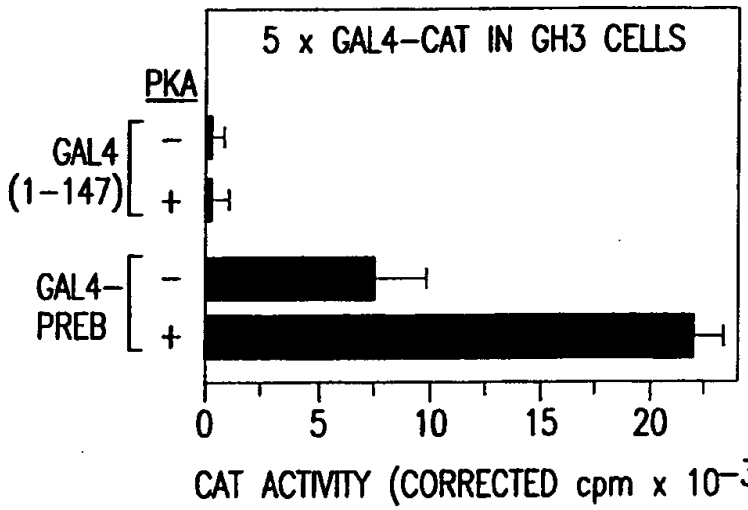

5 x GAL4-CAT IN GH3 CELLS
PKA
GAL4
(1-147)
-
+
GAL4-
PREB
-
+
0
5
10
15
20
CAT ACTIVITY (CORRECTED cpm x 10-3)

FIG.9

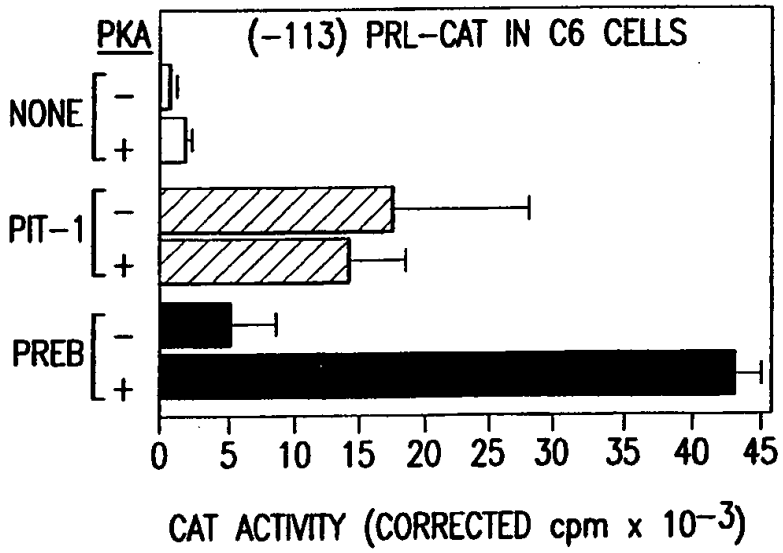

PKA
(-113) PRL-CAT IN C6 CELLS
NONE
PIT-1
PREB
-
+
0 5 10 15 20 25 30 35 40 45
CAT ACTIVITY (CORRECTED cpm x 10^{-3})

FIG.10

```
1 TGGCAACTCCCCGGTGTGAGAGGGGTAGGGAGTGCTCCCGGCGGCGACGGGGCCGAGTTC
  ACCAGCCGCCGGGGCAGTAGTCGAAGGCCCGGCGCGGCATGTCCTGGGTGCCGCGGTGCG
  GGCAGTGAACGCGCGCCCGGGCGGGATGGGCCCGGCGCCGGGCGCCAGAGCTGTACCGGGCT
                          M  G  R  R  R  A  P  E  L  Y  R  A  12
  CCGTTCCCGTTGTACGCGCTTCAGGTCGACCCCAGCACTGGGCTGCTCATCGCTGCGGGC
  P  F  P  L  Y  A  L  Q  V  D  P  S  T  G  L  L  I  A  A  G  32
  GGAGGAGGCGCCGCCAAGACAGGCATAAAGAATGGCGTCCACTTTCTGCAGCTAGAGCTG
  G  G  G  A  A  K  T  G  I  K  N  G  V  H  F  L  Q  L  E  L  52
  ATTAATGGGCGCTTGAGTGCCTCCTTGCTGCACTCCCATGACACAGAGACACGGGCCACC
  I  N  G  R  L  S  A  S  L  L  H  S  H  D  T  E  T  R  A  T  72
  ATGAACTTGGCACTGGCTGGTGACATCCTTGCTGCAGGGCAGGATGCCCACTGTCAGCTC
  M  N  L  A  L  A  G  D  I  L  A  A  G  Q  D  A  H  C  Q  L  92
  CTGCGCTTCCAGGCACATCAACAGCAGGGCAACAAGGCAGAGAAGGCCCGTTCCAAGGAG
  L  R  F  Q  A  H  Q  Q  Q  G  N  K  A  E  K  A  G  S  K  E  112
  CAGGGGCCTCGACAAAGGAAGGGAGCAGCCCCAGCAGAGAAGAAATGTGGAGCGGAAACC
  Q  G  P  R  Q  R  K  G  A  A  P  A  E  K  K  C  G  A  E  T  132
  CAGCACGAGGGGCTAGAACTCAGGGTAGAGAATTTGCAGGCGGTGCAGACAGACTTTAGC
  Q  H  E  G  L  E  L  R  V  E  N  L  Q  A  V  Q  T  D  F  S  152
  TCCGATCCACTGCAGAAAGTTGTGTGCTTCAACCACGATAATACCCTGCTTGCCACTGGA
  S  D  P  L  Q  K  V  V  C  F  N  H  D  N  T  L  L  A  T  G  172
  GGAACAGATGGCTACGTCCGTGTCTGGAAGGTGCCCAGCCTGGAGAAGGTTCTGGAGTTC
  G  T  D  G  Y  V  R  V  W  K  V  P  S  L  E  K  V  L  E  F  192
  AAAGCCCACGAAGGGGAGATTGAAGACCTGGCTTTAGGGCCTGATGGCAAGTTGGTAACC
  K  A  H  E  G  E  I  E  D  L  A  L  G  P  D  G  K  L  V  T  212
  GTGGGCCGGGACCTTAAGGCCTCTGTGTGGCAGAAGGATCAGCTGGTGACACAGCTGCAC
  V  G  R  D  L  K  A  S  V  W  Q  K  D  Q  L  V  T  Q  L  H  232
  TGGCAAGAAAATGGACCCACCTTTTCCAGCACACCTTACCGCTACCAGGCCTGCAGGTTT
  W  Q  E  N  G  P  T  F  S  S  T  P  Y  R  Y  Q  A  C  R  F  252
  GGGCAGGTTCCAGACCAGCCTGCTGGCCTGCGACTCTTCACAGTGCAAATTCCCCACAAG
  G  Q  V  P  D  Q  P  A  G  L  R  L  F  T  V  Q  I  P  H  K  272
  CGCCTGCGCCAGCCCCCTCCCTGCTACCTCACAGCCTGGGATGGCTCCAACTTCTTGCCC
  R  L  R  Q  P  P  P  C  Y  L  T  A  W  D  G  S  N  F  L  P  292
  CTTCGGACCAAGTCCTGTGGCCATGAAGTCGTCTCCTGCCTCGATGTCAGTGAATCCGGC
  L  R  T  K  S  C  G  H  E  V  V  S  C  L  D  V  S  E  S  G  312
  ACCTTCCTAGGCCTGGGCACAGTCACTGGCTCTGTTGCCATCTACATAGCTTTCTCTCTC
  T  F  L  G  L  G  T  V  T  G  S  V  A  I  Y  I  A  F  S  L  332
  CAGTGCCTCTACTACGTGAGGGAGGCCCATGGCATTGTGGTGACGGATGTGGCCTTTCTA
  Q  C  L  Y  Y  V  R  E  A  H  G  I  V  V  T  D  V  A  F  L  352
  CCTGAGAAGGGTCGTGGTCCAGAGCTCCTTGGGTCCCATGAAACTGCCCTGTTCTCTGTG
  P  E  K  G  R  G  P  E  L  L  G  S  H  E  T  A  L  F  S  V  372
  GCTGTGGACAGTCGTTGCCAGCTGCATCTGTTGCCCTCACGGCGGAGTGTTCCTGTGTGG
  A  V  D  S  R  C  Q  L  H  L  L  P  S  R  R  S  V  P  V  W  392
  CTCCTGCTCCTGCTGTGTGTCGGGCTTATTATTGTGACCATCCTGCTGCTCCAGAGTGCC
  L  L  L  L  L  C  V  G  L  I  I  V  T  I  L  L  L  Q  S  A  412
  TTTCCAGGTTTCCTTTAGCTTCCCTGCTTCCTGGGAATCAGGAGCCTGGACACTGCCATC
  F  P  G  F  L  *
```

FIG. 11A

TCTAGAGCAGAGTGGAGGCCTGGACTCCCTTTGCTCACTCCATTCGGGTCCACAGCTGAG
GTTGCCTCTGACAAGATGAATGGGCACTGCCTGCCCTTCTAGTGAAAAGGCTTGGCTATG
GCCCTGTGTGACTCCAGGTCCCAGGAACCTTGCCTTCGTCATCTGTGGATCCATCCAGAA
CAGCGGTATCTGAAGCCCAGGCCATACTCCCTGCCTCCTTTCTTCTGCCTACCAGAGGCT
CCAGAGTTGAGCTTGTCCTTATCTAGAAACATGTGAAGATGCCCAAGAGCCTGGAGGCAC
TGCTGTCCTTCCTGCAGAAACAGTTTCTCCTCCTCCCCTCAGCCTTGTGGCCAGTTCCTC
TTCACATGAAGCCCCTGGCATTTGCTGGGGAAGGGACTGGCCTGGTACTTGCTGTTAGGG
CAGGAAGGGGCAAAAGGAAGACTTGGGTAGTAATCTGGGGGTTCAGATGGGTAGCACTAA
GCCAGCTGGCCTAAAGATGCAATAAGTTCCTAGGTAGTCTACCCTTACCTTGAGGAATGG
GAAAATGAACCTCAGCCCATTAGGCAGGAAAAGTTGATATTTAATAAACAAGGAAAGAGT
GAACTTGAGACCCCAAAAAAAAAAAAAAAAAA 2072

FIG. 11B

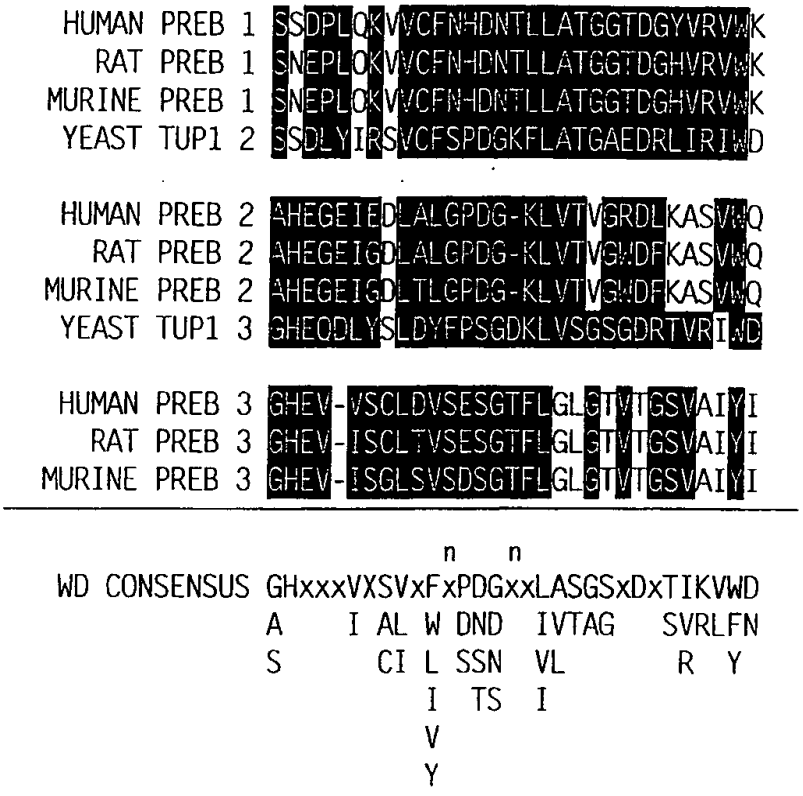

HUMAN PREB 1 SSDPLQKVVCFNHDNTLLATGGTDGYVRVWK
RAT PREB 1 SNEPLQKVVCFNHDNTLLATGGTDGHVRVWK
MURINE PREB 1 SNEPLQKVVCFNHDNTLLATGGTDGHVRVWK
YEAST TUP1 2 SSDLYIRSVCFSPDGKFLATGAEDRLIRIWD
HUMAN PREB 2 AHEGEIEDLALGPDG-KLVTVGRDLKASVWQ
RAT PREB 2 AHEGEIGDLALGPDG-KLVTVGWDFKASVWQ
MURINE PREB 2 AHEGEIGDLTLGPDG-KLVTVGWDFKASVWQ
YEAST TUP1 3 GHEQDLYSLDYFPSGDKLVSGSGDRTVRIWD
HUMAN PREB 3 GHEV-VSCLDVSESGTFLGLGTVTGSVAIYI
RAT PREB 3 GHEV-ISCLTVSESGTFLGLGTVTGSVAIYI
MURINE PREB 3 GHEV-ISGLSVSDSGTFLGLGTVTGSVAIYI
n n
WD CONSENSUS GHxxxVXSVxFxPDGxxLASGSxDxTIKVWD
A I AL W DND IVTAG SVRLFN
S CI L SSN VL R Y
I TS I
V
Y

FIG.12

	1	2	3	4	5	6	7	8
A	WHOLE BRAIN	AMYGDALA	CAUDATE NUCLEUS	CEREBELLUM	CEREBRAL CORTEX	FRONTAL LOBE	HIPPO-CAMPUS	MEDULLA OBLONGATA
B	OCCIPITAL LOBE	PUTAMEN	SUBSTANTIA NIGRA	TEMPORAL LOBE	THALAMUS	NUCLEUS ACCUMBEUS	SPINAL CORD	
C	HEART	AORTA	SKELETAL MUSCLE	COLON	BLADDER	UTERUS	PROSTATE	STOMACH
D	TESTIS	OVARY	PANCREAS	PITUITARY GLAND	ADRENAL GLAND	THYROID GLAND	SALIVARY GLAND	MAMMARY GLAND
E	KIDNEY	LIVER	SMALL INTESTINE	SPLEEN	THYMUS	PERIPHERAL LEUKOCYTE	LYMPH NODE	BONE MARROW
F	APPENDIX	LUNG	TRACHEA	PLACENTA				
G	FETAL BRAIN	FETAL HEART	FETAL KIDNEY	FETAL LIVER	FETAL SPLEEN	FETAL THYMUS	FETAL LUNG	
H	YEAST TOTAL RNA 100ng	YEAST tRNA 100ng	*E-coli* rRNA 100ng	*E-coli* DNA 100ng	POLY r(A) 100ng	HUMAN $C_o t1$ DNA 100ng	HUMAN DNA 100ng	HUMAN DNA 500ng

FIG. 13A

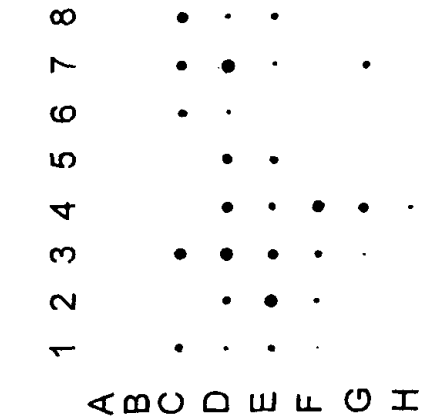


FIG.13D

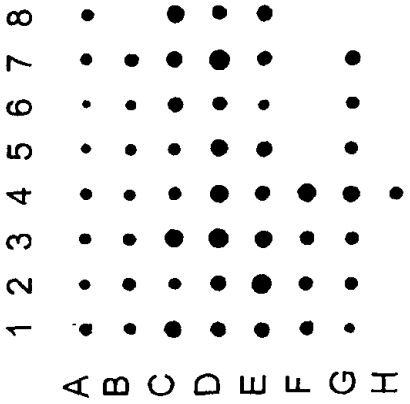


FIG.13C

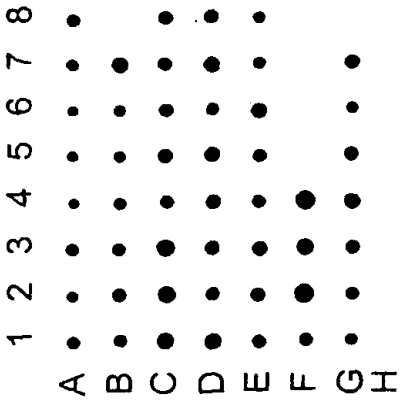


FIG.13B

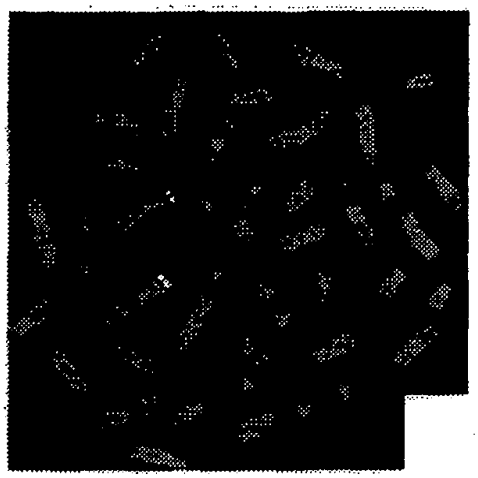


FIG.14A

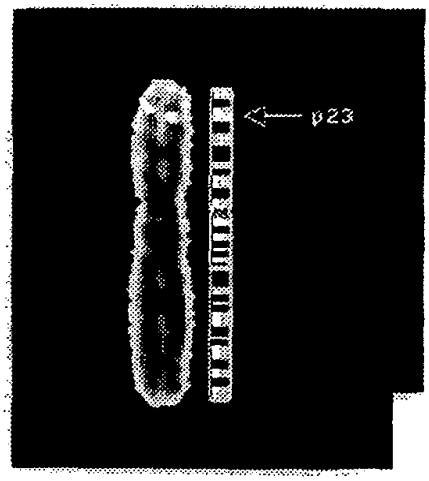


FIG.14B

FIG.14C

FIG.14D

FIG.14E

FIG.14F

FIG.14G

```
   1  TGGCAACTCC CCGGTGTGAG AGGGGTAGGG AGTGCTCCCG GCGGCGACGG
  51  GGCCGAGTTC ACCAGCCGCC GGGGCAGTAG TCGAAGGCCC GGCGCGGCAT
 101  GTCCTGGGTG CCGCGGTGCG GGCAGTGAAC GCGCGCCGGG CGGGATGGGC
 151  CGGCGCCGGG CGCCAGAGCT GTACCGGGCT CCGTTCCCGT TGTACGCGCT
 201  TCAGGTCGAC CCCAGCACTG GGCTGCTCAT CGCTGCGGGC GGAGGAGGCG
 251  CCGCCAAGAC AGGCATAAAG AATGGCGTGC ACTTTCTGCA GCTAGAGCTG
 301  ATTAATGGGC GCTTGAGTGC CTCCTTGCTG CACTCCCATG ACACAGAGAC
 351  ACGGGCCACC ATGAACTTGG CACTGGCTGG TGACATCCTT GCTGCAGGGC
 401  AGGATGCCCA CTGTCAGCTC CTGCGCTTCC AGGCACATCA ACAGCAGGGC
 451  AACAAGGCAG AGAAGGCCGG TTCCAAGGAG CAGGGGCCTC GACAAAGGAA
 501  GGGAGCAGCC CCAGCAGAGA AGAAATGTGG AGCGGAAACC CAGCACGAGG
 551  GGCTAGAACT CAGGGTAGAG AATTTGCAGG CGGTGCAGAC AGACTTTAGC
 601  TCCGATCCAC TGCAGAAAGT TGTGTGCTTC AACCACGATA ATACCCTGCT
 651  TGCCACTGGA GGAACAGATG GCTACGTCCG TGTCTGGAAG GTGCCCAGCC
 701  TGGAGAAGGT TCTGGAGTTC AAAGCCCACG AAGGGGAGAT TGAAGACCTG
 751  GCTTTAGGGC CTGATGGCAA GTTGGTAACC GTGGGCCGGG ACCTTAAGGC
 801  CTCTGTGTGG CAGAAGGATC AGCTGGTGAC ACAGCTGCAC TGGCAAGAAA
 851  ATGGACCCAC CTTTTCCAGC ACACCTTACC GCTACCAGGC CTGCAGGTTT
 901  GGGCAGGTTC CAGACCAGCC TGCTGGCCTG CGACTCTTCA CAGTGCAAAT
 951  TCCCCACAAG CGCCTGCGCC AGCCCCCTCC CTGCTACCTC ACAGCCTGGG
1001  ATGGCTCCAA CTTCTTGCCC CTTCGGACCA AGTCCTGTGG CCATGAAGTC
1051  GTCTCCTGCC TCGATGTCAG TGAATCCGGC ACCTTCCTAG GCCTGGGCAC
1101  AGTCACTGGC TCTGTTGCCA TCTACATAGC TTTCTCTCTC CAGGGAGTGT
1151  TCCTGTGTGG CTCCTGCTCC TGCTGTGTGT CGGGCTTATT ATTGTGACCA
1201  TCCTGCTGCT CCAGAGTGCC TTTCCAGGTT TCCTTTAGCT TCCCTGCTTC
1251  CTGGGAATCA GGAGCCTGGA CACTGCCATC TCTAGAGCAG AGTGGAGGCC
1301  TGGACTCCCT TTGCTCACTC CATTCGGGTC CACAGCTGAG GTTGCCTCTG
1351  ACAAGATGAA TGGGCACTGC CTGCCCTTCT AGTGAAAAGG CTTGGCTATG
1401  GCCCTGTGTG ACTCCAGGTC CCAGGAACCT TGCCTTCGTC ATCTGTGGAT
1451  CCATCCAGAA CAGCGGTATC TGAAGCCCAG GCCATACTCC CTGCCTCCTT
1501  TCTTCTGCCT ACCAGAGGCT CCAGAGTTGA GCTTGTCCTT ATCTAGAAAC
1551  ATGTGAAGAT GCCCAAGAGC CTGGAGGCAC TGCTGTCCTT CCTGCAGAAA
1601  CAGTTTCTCC TCCTCCCCTC AGCCTTGTGG CCAGTTCCTC TTCACATGAA
1651  GCCCCTGGCA TTTGCTGGGG AAGGGACTGG CCTGGTACTT GCTGTTAGGG
1701  CAGGAAGGGG CAAAAGGAAG ACTTGGGTAG TAATCTGGGG GTTCAGATGG
1751  GTAGCACTAA GCCAGCTGGC CTAAAGATGC AATAAGTTCC TAGGTAGTCT
1801  ACCCTTACCT TGAGGAATGG GAAAATGAAC CTCAGCCCAT TAGGCAGGAA
1851  AAGTTGATAT TTAATAAACA AGGAAAGAGT GAACTTGAGA CCCCAAAAAA
1901  AAAAAAAAAA AA
```

FIG. 15A

```
  1  MGRRRAPELY RAPFPLYALQ VDPSTGLLIA AGGGGAAKTG IKNGVHFLQL
 51  ELINGRLSAS LLHSHDTETR ATMNLALAGD ILAAGQDAHC QLLRFQAHQQ
101  QGNKAEKAGS KEQGPRQRKG AAPAEKKCGA ETQHEGLELR VENLQAVQTD
151  FSSDPLQKVV CFNHDNTLLA TGGTDGYVRV WKVPSLEKVL EFKAHEGEIE
201  DLALGPDGKL VTVGRDLKAS VWQKDQLVTQ LHWQENGPTF SSTPYRYQAC
251  RFGQVPDQPA GLRLFTVQIP HKRLRQPPPC YLTAWDGSNF LPLRTKSCGH
301  EVVSCLDVSE SGTFLGLGTV TGSVAIYIAF SLQGVFLCGS CSCCVSGLLL
```

FIG. 15B

GGATCCCCATGTTGCCCAGGCTGTCTCGAAAGCCTGGGCTCAAGCCATCCTCCTCTCTCGGACTTTCCGAAAGTGTTGGGATTACAGGAGGATTACAGGCATGAACCACCG
TGCCTGGCAGAGGATTTTTTTTTTTTTTTGAGACGGAGTTTCACTCTTGTTGCTTGTTGCCCAGGCTGAAGAGCAATGGCAATGGCGCGATCTCGGCTCACTGCAACCTCTA
CTTCCCAGGTTCAAGTGATTCTCCTGCCTCAGGCTCCCGAGTAGCTGGGATTACAGGCGCACGCCACCACGCCCTTTGTATTTTTGGTAGAGACGGGGTTTCTCCATGTTG
GTCAGGCTGGTCTCGAACTCCTGATCCGCCCGCCTAGGACTCACAAAGTGCTGGGATTACAGGCGCGAGTCGGATTTCTTTATTAAAGGTTGACCTTCATCAACCTCCATT
GGGTCCACCTCCTCCGCCCGCGCCCCGCGCCCCGCACAAAAATGGCGAAGTCGGTGCTGGGCGACTCTGCCTCCGCGCCAGGGGTGGAGAACCGAAGCCCCGCCCCGGGAA
ACGCCGCCCCGCGGCCGGCTAGTGCTGACGCGTGTCGGCGCTCCTGCGCCTGCGCGGAGGGAGCCGCGAGACAGGTGCGCATGCGCAATGCGCGTCTGCGAGAACGACTTG
GACGGGAGCCGACCTGAGGCTCCGCTTCCTGCTGATGGTCAAGGGTTT
TGGCAACTCCCCGGTGTGAGAGGGGTAGGGAGTGCTCCCGGCGGCGACGGGGCCGAGTTCACCAGCCGCCGGGGCAGTAG
TCGAAGGCCCGGCGCGGCATGTCCTGGGTGCCGCGGTGCGGGCAGTGAACGCGCGCCGGG
CGGGATGGGCCGGCGCCGGGCGCCAGAGCTGTACCGGGCTCCGTTCCCGTTGTACGCGCTTCAGGTCGACCCCAGCACTG
GGCTGCTCATCGCTGCGGGCGGAGGAGGCGCCGCCAAGACAGGCATAAAGAATGGCGTG
GTGAGAGCGCAGGGCCACTGGGGCTGGGTCTTGCTGCGGGCTGGCGGCGATTCCAAGGTGGCCGGGGGGTCGCGGGGCGGGCCACACTCCAGCTTCGGGCCCTGCCCACTT
CTGTTGGGAAGACCCGCTTGCCTGACGCCCAGGGGCGAATTTCAGTCGAGAACTCAGGCGGGCGGAGGAGAGGCTTTTAAGGTAAAGTGAAAACTGCACACAGCTGCAGAG
TCGCGAGGAACGCTTCAGCTCCGCCTCAGAACAGCTCCAGGGGTCTTATACTGGCCTTTTCCGGGAGGTCTTGCCTGCCCTCTAGCAGCGGCGAGAGTGGTGCATTTGGGT
TTAAGCTAAGTTCCTTCCCTCTCCTGAGCTTAACCTGTTCTGTAAAATAAAGGTAATAATCCCAATCCTGCTCACTGTGTATATTTGTGAGGCCCAAATGAGAAAAAAAAAG
ACTCGAGAAAACCTTGTGAACTAAAACGTGCAAAAAACAAAAGGGGTAAAACATCAGACTCTTCCCTAAACGTGCTCTCTGGGGCACCCCTGAAATTGCTCATCCGGGTTC
CCCCTCCCACAG
CACTTTCTGCAGCTAGAGCTGATTAATGGGCGCTTGAGTGCCTCCTTGCTGCACTCCCATGACACAGAGAC
ACGGGCCACCATGAACTTGGCACTGGCTGGTGACATCCTTGCTGCAGGGCAGGATGCCCACTGTCAGCTCCTGCGCTTCC
AGGCACATCAACAGCAGGGCAACAAGGCAGAGAAGGCCG
GTTGAGGACTCCCTTTTTTACCCCCTTTGGGAAAGGGTTGAACGAGNAAGTCACTCTTTGTGT
CTCTAAAGAAGTTGGTCTTGAAGTAGGTTTTGTAGCAAGCTAGAAGTTGTTTGGGCACCTGCCATTGGAGAGGAGGGGCC
AGTACTCCTTACTGTAGAAGCTTGAACCTGGCCAAGTGTTTGTGTTACAG
GTTCCAAGGAGCAGGGGCCTCGACAAAGGAAGGGAGCAGCCCCAGCAGAGAAGAAATGTGGAGCGGAAACC
CAGCACGAGGGGCTAGAACTCAGGGTAGAGAATTTGCAGGCGGTGCAGACAGACTTTAGCTCCGATCCACTGCAGAAAGTTGTGTGCTTCAACCACGATAATACCCTGCTT
GCCACTGGAGGAACAGATGGCTACGTCCGTGTCTGGAAG

FIG.16A

GTGTGGGTTTGCAGGGTTAGGGAGGGTGAATGTCAGTAGCAACAGGATCAAAATTGTGAGAAGTTGAACGTGGCATCTG
GGAAACTTGTGAATGAAGCTTGCATTGAGGGGCCATTAGAAGGGGTGGCGTGGGCATCAGTCACAGTGTACTTGCTGGACACCTGAGTTAACCATGGTGGTTGTTTGGCTACAG
GTGCCCAGCCTGGAGAAGGTTCTGGAGTTCAAAGCCCACGAAGGGGAGATTGAAGACCTGGCTTTAGGGCCTGATGGCAAG
GTGAGGGGCTGGGGGTGGGAGGAGGATGGAGAAAGGAGAGAGGAGGTGCTTATGCTGCTTGCCCAGTAAGTGGAT
CCCCTAACTGTCCATCCTTGGAATCTTTATTCCTAACTAG
TTGGTAACCGTGGGCCGGGACCTTAAGGCCTCTGTGTGGCAGAAGGATCAGCTGGTGACACAGCTGCACTGGCAAGAAA
ATGGACCCACCTTTTCCAGCACACCTTACCGCTACCAGGCCTGCAG
GTGTGAAGACTTTGGGGGGTGGCTGAAAGAGGCATAGCCCAGCTGTGGTGGGGGAGAGGGAAAAGACTGGGGATG
GGAGAGCTGGGGAGGAACTTGTTGAGTGTTACCCCAGGTCTGACCAGGGTGCAGGTGGTGCACAAACCTCTGAGGAGGGT
TGGGCAGGCCCTANGAGCTGAATAACCCCTCATCCGGCCCCCAG
GTTTGGGCAGGTTCCAGACCAGCCTGCTGGCCTGCGACTCTTCACAGTGCAAATTCCCCACAAGCGCCTGCGCC
AGCCCCCTCCCTGCTACCTCACAGCCTGGGATGGCTCCAACTTCTTGCCCCTTCGGACCAAGTCCTGTGGCCATGAAGTCGTCTCCTGCCTCGATGTCAG
GTGTTAGACATTGCTGCCTTGGGCTAGGTAGGGGGTCCCTGAGGGAGCTTGGAAAGGAGTCCTGCCTGGGT
CCCTACGGACCGGTATTGGGGTATGAGGGTTGCTGCACAAGCCTCCAGGACAATGAGCTCTTTATTGTTTGTTGCAG
TGAATCCGGCACCTTCCTAGGCCTGGGCACAGTCACTGGCTCTGTTGCCATCTACATAGCTTTCTCTCTCCAG
GTAATGGGTGGAGGTTGGCATGGCCCTGTGGGTGGACTGTAGGCCTGTCTCTACCCTGAGTTTGCAGGAAGGAGTCTGGC
CCATCCTATCGAGGGAAATCCTGGGGGTGGGGAACATGCTTTCCAGAAAGAGAGTTCCCAGCTAGGCCTTTCCTCACTGG TATTCCTTCTGCCCACAG
TGCCTCTACTACGTGAGGGAGGCCCATGGCATTGTGGTGACGGATGTGGCCTTTCTACCTGAGAAGGGTCGTGGTCC
AGAGCTCCTTGGGTCCCATGAAACTGCCCTGTTCTCTGTGGCTGTGGACAGTCGTTGCCAGCTGCATCTGTTGCCCTCACGGC
GTGAGTCATTGGGGCAGGGCAGGCAGGCACCACCCCACGTTTAATGACCAGAAACGTGCCCCCCGGAGGCTGG
GCTCTTTGTGCCACTCCTCCTTTGAAGGGTTCTGGTTTTCAGGCTGGGAAGCCCTTTTGCCCGCTGACCTCCTCCCTTTCCCTCCTGCAG
GGAGTGTTCCTGTGTGGCTCCTGCTCCTGCTGTGTGTCGGGCTTATTATTGTGACCATCCTGCTGCTCCAGAGTGCCTTTCCAGGTTTCCTTTAGCTTCCCTGCTTCCTGG
GAATCAGGAGCCTGGACACTGCCATCTCTAGAGCAGAGTGGAGGCCTGGACTCCCTTTGCTCACTCCATTCGGGTCCACAGCTGAGGTTGCCTCTGACAAGATGAATGGGC
ACTGCCTGCCCTTCTAGTGAAAAGGCTTGGCTATGGCCCTGTGTGACTCCAGGTCCCAGGAACCTTGCCTTCGTCATCTGTGGATCCATCCAGAACAGCGGTATCTGAAGC
CCAGGCCATACTCCCTGCCTCCTTTCTTCTGCCTACCAGAGGCTCCAGAGTTGAGCTTGTCCTTATCTAGAAACATGTGAAGATGCCCAAGAGCCTGGAGGCACTGCTGTC
CTTCCTGCAGAAACAGTTTCTCCTCCTCCCCTCAGCCTTGTGGCCAGTTCCTCTTCACATGAAGCCCCTGGCATTTGCTGGGGAAGGGACTGGCCTGGTACTTGCTGTTAG
GGCAGGAAGGGGCAAAAGGAAGACTTGGGTAGTAATCTGGGGGTTCAGATGGGTAGCACTAAGCCAGCTGGCCTAAAGATGCAATAAGTTCCTAGGTAGTCTACCCTTACC
TTGAGGAATGGGAAAATGAACCTCAGCCCATTAGGCAGGAAAAGTTGATATTTAATAAACAAGGAAAGAGTGAACTTGAGACC

FIG.16B

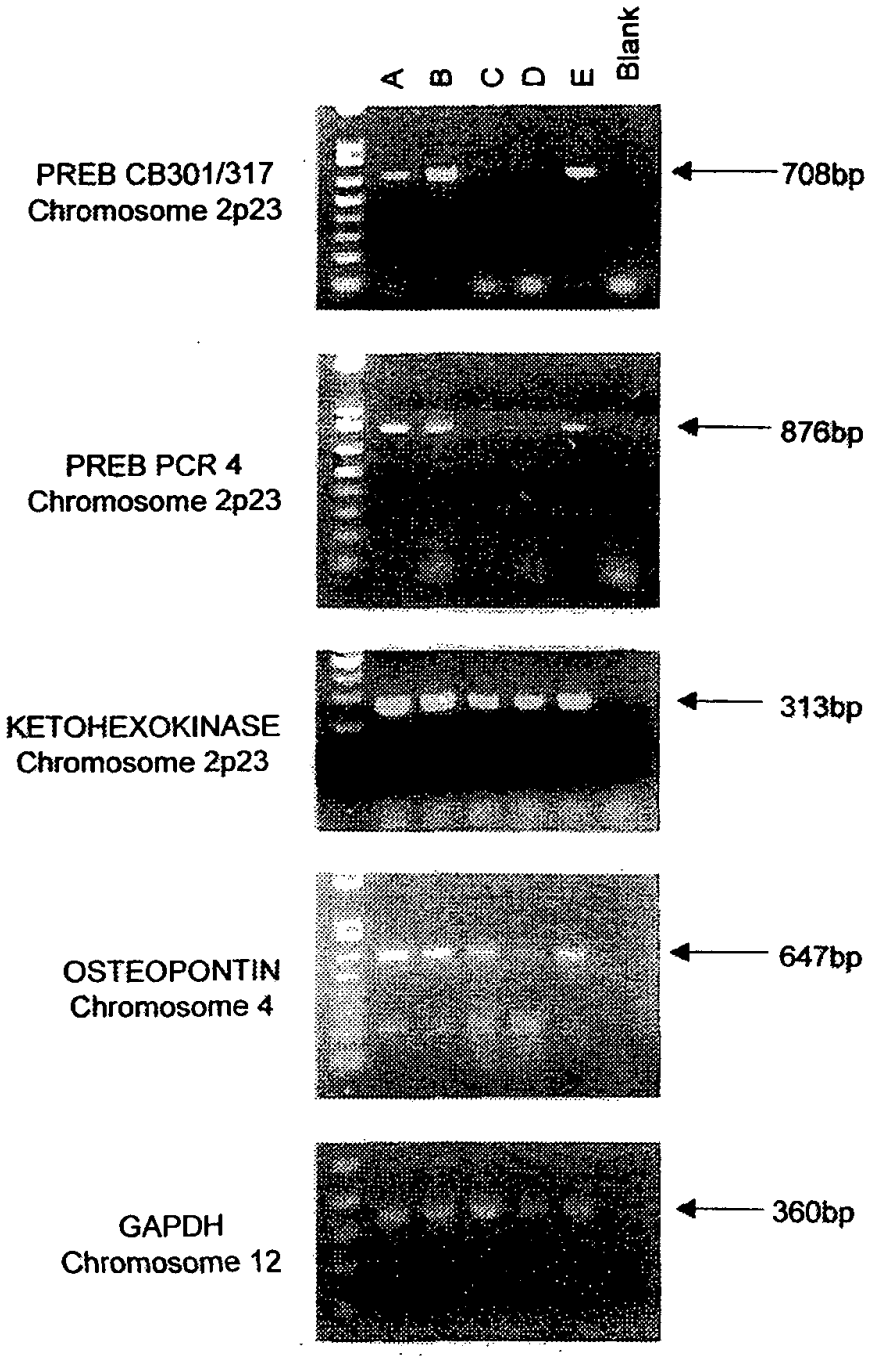

A
B
C
D
E
Blank
PREB CB301/317
Chromosome 2p23
708bp
PREB PCR 4
Chromosome 2p23
876bp
KETOHEXOKINASE
Chromosome 2p23
313bp
OSTEOPONTIN
Chromosome 4
647bp
GAPDH
Chromosome 12
360bp

FIG. 17